

CC	to treat conditions mediated by the kallikrein-like proteins	PI	Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillian KJ; Klein RD, Gurney AL, Kuo SS, Paoni NF;
XX		PI	Goddard A, Godowski PJ, Smith V, Watanabe CK, Williams PM,
SQ	Sequence 248 AA;	XX	Wood WI;
Query Match	100.0%; Score 1374; DB 3; Length 248;	DR	WPI: 2000-412154/35.
Best Local Similarity	100.0%; Pred. No. 3.8e-98;	N-PSDB:	AAB77671.
Matches 248;	Conservative 0; Mismatches 0;	XX	
Qy	1 MGLSIFILCIGLGSQATPKEFTECGRNSQPWQVGLFEGTSLRGGVLDIHWVITA 60	PT	Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating disorders in mammals.
Db	1 MGLSIFILCIGLGSQATPKEFTECGRNSQPWQVGLFEGTSLRGGVLDIHWVITA 60	PT	PT and treating disorders in cardiovascular, endothelial or angiogenic
Qy	61 AHCGSRWYWRGEHSLSQLDTEQIRSGFATVTHPELGASTSHEDHLRLRLLPVRY 120.	PT	PT and treating disorders in cardiovascular, endothelial or angiogenic
Db	61 AHCGSRWYWRGEHSLSQLDTEQIRSGFATVTHPELGASTSHEDHLRLRLLPVRY 120	PT	disorders in mammals.
Qy	121 TSSVQPLPLPNDCATACTECHVSGKGTINHPRNPPDQLQCLNLSTVSHATCHGTVYPGR 180	XX	The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating disorders in cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation.
Db	121 TSSVQPLPLPNDCATACTECHVSGKGTINHPRNPPDQLQCLNLSTVSHATCHGTVYPGR 180	XX	and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertension). For example, the nucleic acids (Ncs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAB77510 to AAA77721 and AAB24388 to AAB24435 represent nucleotide and protein sequences used in the exemplification of the present invention.
Qy	181 TSNMVCAGGVPQDACQDSGPVLVCCGVLQCLVSGCSVGCGQOCIPGVYTYICKVDW 240	XX	XX
Db	181 TSNMVCAGGVPQDACQDSGPVLVCCGVLQCLVSGCSVGCGQOCIPGVYTYICKVDW 240	XX	Sequence 248 AA;
Qy	241 IRMIMANN 248	SQ	Query Match 100.0%; Score 1374; DB 3; Length 248;
Db	241 IRMIMANN 248	Best Local Similarity 100.0%; Pred. No. 3.8e-98;	
AC	AAB24428 standard; protein; 248 AA.	Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DT	07-NOV-2000 (first entry)	Db	1 MGLSIFILCIGLGSQATPKEFTECGRNSQPWQVGLFEGTSLRGGVLDIHWVITA 60
XX	Human PRO1303 Protein sequence SEQ ID NO:203.	Qy	61 AHCGSRWYWRGEHSLSQLDTEQIRSGFATVTHPELGASTSHEDHLRLRLLPVRY 120
KW	Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.	Db	61 AHCGSRWYWRGEHSLSQLDTEQIRSGFATVTHPELGASTSHEDHLRLRLLPVRY 120
KW	Homo sapiens.	Qy	121 TSSVQPLPLPNDCATACTECHVSGKGTINHPRNPPDQLQCLNLSTVSHATCHGTVYPGR 180
OS		Db	121 TSSVQPLPLPNDCATACTECHVSGKGTINHPRNPPDQLQCLNLSTVSHATCHGTVYPGR 180
PN	WO2000032221-A2.	Qy	181 TSNMVCAGGVPQDACQDSGPVLVCCGVLQCLVSGCSVGCGQOCIPGVYTYICKVDW 240
XX		Db	181 TSNMVCAGGVPQDACQDSGPVLVCCGVLQCLVSGCSVGCGQOCIPGVYTYICKVDW 240
PD	08-JUN-2000.	Qy	241 IRMIMANN 248
XX		Db	241 IRMIMANN 248
PF	30-NOV-1999; 99WO-US028313.	RESULT 3	AAB24032
XX		ID	AAB24032 standard; protein; 248 AA.
PR	01-DEC-1998; 98WO-US025108.	XX	
PR	16-DEC-1998; 98US-0112850P.	AC	AAB24032;
PR	12-JAN-1999; 99US-015554P.	XX	
PR	08-MAR-1999; 99WO-US005028.	DT	25-JAN-2001 (first entry)
PR	12-MAR-1999; 99US-0123957P.	XX	Human PRO1303 protein sequence SEQ ID NO:33.
PR	28-JUL-1999; 99US-013445P.	DB	
PR	14-MAY-1999; 99US-0134287P.	XX	
PR	02-JUN-1999; 99WO-US012252.	AC	
PR	23-JUN-1999; 99US-01037P.	XX	
PR	20-JUL-1999; 99US-0144758P.	DT	
PR	26-JUL-1999; 99US-0145638P.	XX	
PR	01-SEP-1999; 99WO-US022011.	DB	
PR	08-SEP-1999; 99WO-US020591.	XX	
PR	13-SEP-1999; 99WO-US020544.	KW	Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
PR	15-SEP-1999; 99WO-US01090.	KW	identification; tumorigenesis; anticancer; detection.
PR	15-SEP-1999; 99WO-US021547.	XX	
PR	05-OCT-1999; 99WO-US023089.	OS	
PR	29-OCT-1999; 99US-0162506P.	XX	
XX		PN	WO200003750-A1.
PA	(GETH) GENENTECH INC.	XX	

PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-010265P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-010314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-010328P.
 PR 07-OCT-1998; 98US-0103195P.
 PR 07-OCT-1998; 98US-0103196P.
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 PR 08-OCT-1998; 98US-0103633P.
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 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104387P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-010563P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105607P.
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 PR 28-OCT-1998; 98US-0106062P.
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 PR 28-OCT-1998; 98US-0106031P.
 PR 28-OCT-1998; 98US-0106032P.
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 PR 03-NOV-1998; 98US-0106516P.
 PR 03-NOV-1998; 98US-0106202P.
 PR 03-NOV-1998; 98US-0106205P.
 PR 03-NOV-1998; 98US-0106919P.
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 PR 03-NOV-1998; 98US-0106344P.
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 PR 17-NOV-1998; 98US-0106207P.
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 PR 17-NOV-1998; 98US-0108788P.
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 PR 17-NOV-1998; 98US-0108813P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108848P.
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 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108859P.
 XX (GETH) GENENTECH INC.

PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX Claim 12; Fig 108; 773pp; English.

CC AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The CC transmembrane and receptor PRO proteins can be used for screening of CC potential peptide or small molecule inhibitors of the relevant sequences CC receptor/ligand interactions. The polypeptides and nucleotide sequences CC encoding them have various industrial applications, including uses as CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR CC primers and hybridisation probes used in the isolation of the PRO CC polypeptides from the present invention.

XX Sequence 248 AA;

SO Query Match 100.0%; Score 1374; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSPLLICVGLSQAATPKIENTECGRNSNQPPQVGLPECTSARCGGYLIDHWRVLT 60
 Db 1 MGLSPLLICVGLSQAATPKIENTECGRNSNQPPQVGLPECTSARCGGYLIDHWRVLT 60

Qy 61 AHCSGSRYWRLGEISLSQDWTB0TRHSGFSVTIPGVLASTSHEDLRLRLLPVRV 120
 Db 61 AHCSGSRYWRLGEISLSQDWTB0TRHSGFSVTIPGVLASTSHEDLRLRLLPVRV 120

Qy 121 TSSVOPPLPNMDCATAGTCTCHVSGGITINHPRNPPDILQCLNTSLVSHATCHGTYGPRI 180
 Db 121 TSSVOPPLPNMDCATAGTCTCHVSGGITINHPRNPPDILQCLNTSLVSHATCHGTYGPRI 180

Qy 181 TSNNMTCAGGYVGODACQGSGGGPVAIAGGGTVQGLSVPGSVPCGQDGIPGTYTICKYVDW 240
 Db 181 TSNNMTCAGGYVGODACQGSGGGPVAIAGGGTVQGLSVPGSVPCGQDGIPGTYTICKYVDW 240

Qy 241 IRMIRANN 248
 Db 241 IRMIRANN 248

RESULT 5
 AAM23994 standard; protein; 248 AA.
 ID AAM23994;
 AC AAM23994;
 XX -12-OCT-2001 (first entry)
 DB Human EST encoded protein SEQ ID NO: 1519.
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 XX gene therapy; nutrition.
 XX Homo sapiens.

OS XX WO200154477-A2.
 PR XX PR 25-JAN-2000; 2000US-0041404.
 PR XX PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00633870.
 PR XX (HYSE-) HYSEQ INC.
 PR 25-JAN-2001; 2001WO-US002687.
 PR XX PN WO200154477-A2.
 PR XX PR 02-AUG-2001.
 PR XX PR 25-JAN-2001; 2001WO-US002687.
 PR XX (HYSE-) HYSEQ INC.
 PI Baker K., Goddard A., Gurney AL, Smith V., Watanabe CK, Wood WI;
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Weitzman T;

XX DR WPI: 2000-237871/20.
 XX PT New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small PT

cartilage disorder: sports injury: arthritis

cartilage disorder; sports injury; arthritis.		98US-0103449P.
Homo sapiens.		98US-0103314P.
US2003073130-A1.		98US-0103328P.
17-APR-2003.	2001US-00015869.	98US-0103295P.
11-DEC-2001;	2001US-00015869.	98US-0103198P.
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PFR	30-DEC-1998;	98US-0114223P.
PFR	05-JAN-1999;	99W0-US000106.
PFR	16-APR-1999;	99US-0129674P.
PFR	13-JUN-1999;	99US-01144758P.
PFR	20-JUL-1999;	99US-01144759P.

PR	26-JUL-1999;	99US-0145698P.
PR	01-SEP-1999;	99NO-US020111.
PR	15-SEP-1999;	99NO-US021194.
PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99NO-US028313.
PR	02-DEC-1999;	99NO-US028551.
PR	16-DEC-1999;	99NO-US030095.
PR	06-JAN-2000;	2000NO-US000219.
PR	11-FEB-2000;	2000NO-US000376.
PR	18-FEB-2000;	2000NO-US035365.
PR	24-FEB-2000;	2000NO-US004342.
PR	02-MAR-2000;	2000NO-US004004.
PR	15-MAY-2000;	2000NO-US06884.
PR	17-MAY-2000;	2000NO-US013705.
PR	22-MAY-2000;	2000NO-US014042.
PR	30-MAY-2000;	2000NO-US014941.
PR	02-JUN-2000;	2000NO-US015264.
PR	23-AUG-2000;	2000NO-US023522.
PR	24-AUG-2000;	2000NO-US023328.
PR	08-NOV-2000;	2000NO-US030952.
PR	10-NOV-2000;	2000NO-US030873.
PR	01-DEC-2000;	2000NO-US032678.
PR	28-FEB-2001;	2001NO-US06520.
PR	01-MAR-2001;	2001NO-US06666.
PR	01-JUN-2001;	2001NO-US017800.
PR	20-JUN-2001;	2001NO-US011929.
PR	29-JUN-2001;	2001NO-US010166.
PR	09-JUL-2001;	2001NO-US021735.
PR	04-SEP-2001;	2001US-US0946374.
XXX	(GETH) GENENTECH INC.	
Baker KB,	Bottstein D,	Desnoy
Gao W,	Goddard A,	Godowski P
Pan J,	Paroni NP,	Roy MA,
Williams PM,	Wood WI,	Sm
WPTI;	2003-492259/46.	
DDR	N-PSDB;	ACH04480.
XX	Novel secreted and transmembrane	
XX	encoding them useful for treat-	
XX	disorders, bone and/or cartila-	
XX	artitis.	
Query	Query Match	100.0 %;
QPA	Best local Similarity	100.0 %;
QPA	Matches 248; Conservative 0;	
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Ddb	61 AHCGSSRYWVLGHLSLSQD	
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Ddb	121 TSSYQPLPNDCATGTECK	
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Ddb	181 TSNNYCAGGYGVPQDAGCQGDSC	
Qy	241 IRMINENN 24 8	
Ddb	241 IRMINENN 24 8	

ID	ABO33512	standard; protein; 248 AA.	98US-0102307P.
XX	XX	98US-0102330P.	98US-0102331P.
AC	XX	98US-0102331P.	98US-0102331P.
XX	DT	17-SEP-2003 (first entry)	98US-0102484P.
XX	DB	Novel human secreted and transmembrane protein PRO1303.	98US-0102484P.
XX	XX	Human: secreted and transmembrane protein; PRO; gene therapy; vaccine; tissue typing; chromosome identification; vaccine.	98US-0102487P.
KW	RW	Human; secreted and transmembrane protein; PRO; gene therapy; vaccine; tissue typing; chromosome identification; vaccine.	98US-0102570P.
OS	XX	Homo sapiens.	98US-0102571P.
PN	US2003073129-A1.		98US-0102684P.
XX	PD	11-APR-2003.	98US-0102687P.
XX	PP	04-SEP-2001; 2001US-00946374.	98US-0102965P.
XX	PR	01-SEP-1998; 98US-0098716P.	98US-0103258P.
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PR	01-SEP-1998; 98US-0098749P.	98US-0103514P.	
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PR	30-DEC-1998; 98US-0114223P.	98US-0114223P.	
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PR	18-OCT-1999;	99US-00403297.				
PR	30-NOV-1999;	99WO-US0281313.				
PR	02-DEC-1999;	99WO-US02851.				
PR	16-DBC-1999;	99WO-US030095.				
PR	05-JAN-2000;	2000WO-US000219.				
PR	06-JAN-2000;	2000WO-US000316.				
PR	11-FEB-2000;	2000WO-US003565.				
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PR	15-MAR-2000;	2000WO-US006894.				
PR	17-MAY-2000;	2000WO-US013705.				
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PR	08-NOV-2000;	2000WO-US030912.				
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PR	28-FEB-2001;	2001WO-US006540.				
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PR	01-JUN-2001;	2001US-00872035.				
PR	01-JUN-2001;	2001WO-US017840.				
PR	14-JUN-2001;	2001US-00882636.				
PR	20-JUN-2001;	2001WO-US019632.				
PR	29-JUN-2001;	2001WO-US021062.				
PR	09-JUL-2001;	2001WO-US021735.				
XX						
PA	(GETH) GENENTECH INC.					
PA	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;	Eaton DL, Ferrara N, Fong S;	Db	98US-0098716P.		
PA	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ;	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ;	Qy	98US-0098723P.		
PA	Pan J, Paoni NP, Roy MA, Stewart TA, Watanabe CK;	Pan J, Paoni NP, Roy MA, Stewart TA, Watanabe CK;		98US-0098749P.		
PA	Williams PM, Wood WI;	Williams PM, Wood WI;		98US-0098750P.		
XX						
DR	N-PSDB; ACD68024.					
XX						
PT	Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.	Best Local Similarity 100.0%;	Score 1374;	DB 7;	Length 248;	
PT	CC The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I), having at least 80% sequence identity to a sequence	Matches 248;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
XX						
PS	Claim 12; Fig 10B; 561pp; English.					
XX						
CC	Query Match 100.0%;	Best Local Similarity 100.0%;	Pred. No. 3.8e-98;			
CC	Matches 248;	Score 1374;	DB 7;	Length 248;		
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Qy	61 AICSGSRWVRLGEHSLSOLDWTEQIRSGFSTVHPGTLGASTSHEDRLRLRLPVRV 120	61 AICSGSRWVRLGEHSLSOLDWTEQIRSGFSTVHPGTLGASTSHEDRLRLRLPVRV 120	PR	17-SEP-1998;	98US-010663P.	
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Db	121 TSSVQLPLNDATAGTCBCHSGWGTTNHPNPFPDLQCLNLISVHATCHGVYFGR 180	121 TSSVQLPLNDATAGTCBCHSGWGTTNHPNPFPDLQCLNLISVHATCHGVYFGR 180	PR	22-SEP-1998;	98US-010666P.	
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 PR 23-SEP-1998; 98US-0101477P.
 PR 24-SEP-1998; 98US-0101739P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
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 PR 30-SEP-1998; 98US-0102571P.
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 PR 01-OCT-1998; 98US-0102687P.
 PR 06-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 07-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103311P.
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 PR 21-OCT-1998; 98US-0105104P.
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 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 98WO-US00106.
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 PR 20-JUL-1999; 98US-0144758P.
 PR 26-JUL-1999; 98US-0145698P.
 PR 01-SEP-1999; 98NO-US00111.
 PR 15-SEP-1999; 98WO-US02111.
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 PR 30-NOV-1999; 98NO-US028213.
 PR 02-DEC-1999; 98NO-US028551.
 PR 16-DEC-1999; 98NO-US030095.
 PR 05-JAN-2000; 2000NO-US00219.
 PR 06-JAN-2000; 2000NO-US00376.
 PR 11-FEB-2000; 2000NO-US003565.
 PR 22-MAY-2000; 2000NO-US014042.
 PR 18-FEB-2000; 2000NO-US014941.
 PR 24-FEB-2000; 2000NO-US05004.
 PR 02-MAR-2000; 2000NO-US05841.
 PR 15-MAR-2000; 2000NO-US06884.
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 PR 02-JUN-2000; 2000NO-US015264.
 PR 24-AUG-2000; 2000NO-US023522.
 PR 08-NOV-2000; 2000NO-US03328.
 PR 10-NOV-2000; 2000NO-US030952.
 PR 10-DEC-2000; 2000NO-US022678.
 PR 28-FEB-2001; 2001IW0-US106520.
 PR 01-MAR-2001; 2001IW0-US06666.
 PR 01-JUN-2001; 2001IW0-US017800.
 PR 20-JUN-2001; 2001IW0-US19692.
 PR 29-JUN-2001; 2001IW0-US021066.
 PR 09-JUL-2001; 2001IW0-US021235.
 PR 04-SEP-2001; 2001IUS-00346374.
 XX (GHTH) GENENTECH INC.

PR 19-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
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 PR 24-FEB-2000; 2000NO-US05004.
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 PR 29-JUN-2001; 2001IW0-US021066.
 PR 09-JUL-2001; 2001IW0-US021235.
 PR 04-SEP-2001; 2001IUS-00346374.
 XX (GHTH) GENENTECH INC.

PI Baker RP, Botstein D, DeNoyers L, Ferrara N, Fong S, Gao W, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Pan J, Paoni NP, Roy MA, Smith V, Stewart RA, Tumas D, Williams PM, Watanabe CK;
 PI (GHTH) GENENTECH INC.

PR Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 12; SEQ ID NO 194; 555pp; English.
 DR N-PSDB: ADC18062.

XX Query Match Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
 PT Matches 248; Conservative 0; Mismatches 0; Gaps 0;

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 CC 1 MGLSFLLICVLGIGSQATPKIFNGTCGRANSQPQVGGLPEGTSLRCGGYLIDHWRVLT A 60

Qy 61 AHCGSSRSYWVRLGEHSLSQLDWTEQIRHSGFSVTMPGYLGASTSHEHDLRLRLPLPVRY 120

PR	10-NOV-1998;	98US-0107783P.	Query Match Score 1374; DB 7;
PR	17-NOV-1998;	98US-0108775P.	Best Local Similarity 100.0%; Pred. No. 3. 8e-98;
PR	17-NOV-1998;	98US-0108779P.	Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	17-NOV-1998;	98US-0108787P.	
PR	17-NOV-1998;	98US-0108788P.	Qy 1 MGLSIPLL-CVGLSQATPKLNGTECGRNNSQPMQVGLFEGTSRLRCGGVLIDERWLVTA 60
PR	17-NOV-1998;	98US-0108801P.	Db 1 MGLSIPLL-CVGLSQATPKLNGTECGRNNSQPMQVGLFEGTSRLRCGGVLIDERWLVTA 60
PR	17-NOV-1998;	98US-0108802P.	
PR	17-NOV-1998;	98US-0108805P.	
PR	17-NOV-1998;	98US-0108807P.	61 AHCSGSRYAVRLGEHSISQLDWTEQIRHSGFSUTHPGVLGASTSHEDDLRLRLPVRV 120
PR	17-NOV-1998;	98US-0108867P.	Db 61 AHCSGSRYAVRLGEHSISQLDWTEQIRHSGFSUTHPGVLGASTSHEDDLRLRLPVRV 120
PR	18-NOV-1998;	98US-0108923P.	
PR	18-NOV-1998;	98US-0108848P.	Qy 121 TSSVQPLPPIPNDCATAGTECHYSGWGTNAPRNPFPDLIQCLNLSIVSHATCHGVYGR 180
PR	18-NOV-1998;	98US-0108849P.	Db 121 TSSVQPLPPIPNDCATAGTECHYSGWGTNAPRNPFPDLIQCLNLSIVSHATCHGVYGR 180
PR	18-NOV-1998;	98US-0108850P.	
PR	18-NOV-1998;	98US-0108851P.	
PR	18-NOV-1998;	98US-0108852P.	
PR	18-NOV-1998;	98US-0108853P.	
PR	18-NOV-1998;	98US-0108904P.	Qy 181 TSNNVCAVGVPGODAACQDSGGPLVCGYLQGLVSGSYGPCCGDGIPGVYTICKYVD 240
PR	22-DEC-1998;	98US-0113296P.	Db 181 TSNNVCAVGVPGODAACQDSGGPLVCGYLQGLVSGSYGPCCGDGIPGVYTICKYVD 240
PR	30-DEC-1998;	98US-0114222P.	
PR	05-JAN-1999;	99WO-US000106.	
PR	16-APR-1999;	99US-0129674P.	Qy 241 IRMIMRNN 248
PR	23-JUN-1999;	99US-0141037P.	Db 241 IRMIMRNN 248
PR	20-JUL-1999;	99US-014755D.	
PR	26-JUL-1999;	99US-0145698P.	
PR	01-SEP-1999;	99WO-US002011.	
PR	15-SEP-1999;	99WO-US001124.	
PR	29-OCT-1999;	99US-0162506P.	RESULT 12
PR	30-NOV-1999;	99WO-US028313.	ADD39786 standard; protein: 248 AA.
PR	02-DEC-1999;	99WO-US08551.	
PR	16-DBC-1999;	99WO-US030055.	
PR	05-JAN-2000;	2000WO-US000219.	
PR	06-JAN-2000;	2000WO-US000216.	
PR	11-FEB-2000;	2000WO-US003565.	
PR	18-FEB-2000;	2000WO-US004342.	
PR	24-FEB-2000;	2000WO-US005004.	
PR	02-MAR-2000;	2000WO-US005841.	
PR	15-MAR-2000;	2000WO-US006884.	
PR	17-MAY-2000;	2000WO-US013705.	
PR	22-MAY-2000;	2000WO-US014042.	
PR	30-MAY-2000;	2000WO-US014941.	
PR	02-JUN-2000;	2000WO-US015264.	
PR	23-AUG-2000;	2000WO-US023522.	
PR	24-AUG-2000;	2000WO-US023328.	
PR	08-NOV-2000;	2000WO-US030952.	
PR	10-NOV-2000;	2000WO-US030873.	
PR	01-DEC-2000;	2000WO-US032678.	
PR	28-FEB-2001;	2001WO-US006520.	
PR	01-MAR-2001;	2001WO-US006666.	
PR	01-JUN-2001;	2001WO-US017800.	
PR	20-JUN-2001;	2001WO-US019622.	
PR	29-JUL-2001;	2001WO-US021066.	
PR	09-JUL-2001;	2001WO-US021735.	
PR	04-SEP-2001;	2001US-00946374.	
XX	PA (GRET) GENENTECH INC.		
XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Hillan KJ, Gurney AL, Grimaldi JC, Godowski PJ, Gurney AL, Hillan KJ, Gurney MA, Stewart TA, Tumas D, Watanabe CK; Pan J, Paoni NF, Roy MA, Smith V, Williams PM, Wood WI;		
XX	DR; ADD7078.		
XX	N-PSDB;		
PT	Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle cells and are useful for treating diabetes or hyper- or hypo-insulinemia.		
PT	Claim 12: SEQ ID NO 194; 553pp; English.		
PT	The invention relates to an isolated PRO polypeptide (secreted or		
PS	08-NOV-2000; 2000WO-US030952.		
XX	10-NOV-2000; 2000WO-US030873.		
PR	01-DEC-2000; 2000WO-US032678.		
CC	28-FBB-2001; 2001WO-US006520.		

Qy	61	AHCSSGRYWRIGEISLSQDWTBQRHSGPSVTHGASTSHEDRLRLRLPVR	120
Db	61	AHCSSGRYWRIGEISLSQDWTBQRHSGPSVTHGASTSHEDRLRLRLPVR	120
Qy	121	TSSVQLPLNDCATAGTCTCAGTGATLQCLNLSTVSHATCHGTYGPGR	180
Db	121	TSSVQLPLNDCATAGTCTCAGTGATLQCLNLSTVSHATCHGTYGPGR	180
Qy	181	TSNNYCAGGYPGQDAQCGDSGGPLVCGGVNQGLVSGVPGQDGIPGNTYICKYVDW	240
Db	181	TSNNYCAGGYPGQDAQCGDSGGPLVCGGVNQGLVSGVPGQDGIPGNTYICKYVDW	240
Qy	241	IRMIRNN 248	
Db	241	IRMIRNN 248	
RESULT 14			
	ADD38353	ADD38353 standard; protein; 248 AA.	
ID	XX		
AC	ADD38353;		
DT	15-JAN-2004	(first entry)	
XX	XX		
DB	Human secreted/transmembrane protein PRO1303.		
XX	XX		
KW	secreted protein; transmembrane protein; PRO; tumour;		
KW	immune response; cardiac insufficiency disorder; calcium flux;		
KW	umbilical vein endothelial cell; bone disorder; cartilage disorder;		
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;		
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;		
KW	dermatitis; herpetiformis; Crohn's disease; thalassaemia.		
XX	XX		
OS	Homo sapiens.		
PX	US2003096955-A1.		
XX	XX		
PD	22-MAY-2003.		
XX	XX		
PF	07-DEC-2001; 2001US-00012755.		
XX	XX		
PR	01-SEP-1998;	98US-0098116P.	
PR	01-SEP-1998;	98US-0098123P.	
PR	01-SEP-1998;	98US-0098149P.	
PR	01-SEP-1998;	98US-0098150P.	
PR	02-SEP-1998;	98US-009803P.	
PR	02-SEP-1998;	98US-009821P.	
PR	02-SEP-1998;	98US-0098443P.	
PR	09-SEP-1998;	98US-0098336P.	
PR	09-SEP-1998;	98US-009896P.	
PR	09-SEP-1998;	98US-009858P.	
PR	09-SEP-1998;	98US-009802P.	
PR	09-SEP-1998;	98US-0098442P.	
PR	10-SEP-1998;	98US-009741P.	
PR	10-SEP-1998;	98US-009754P.	
PR	10-SEP-1998;	98US-009763P.	
PR	10-SEP-1998;	98US-009792P.	
PR	10-SEP-1998;	98US-009808P.	
PR	10-SEP-1998;	98US-009812P.	
PR	10-SEP-1998;	98US-009815P.	
PR	10-SEP-1998;	98US-009816P.	
PR	15-SEP-1998;	98US-010085P.	
PR	15-SEP-1998;	98US-0100388P.	
PR	15-SEP-1998;	98US-0100190P.	
PR	16-SEP-1998;	98US-010054P.	
PR	16-SEP-1998;	98US-010027P.	
PR	16-SEP-1998;	98US-0100661P.	
PR	16-SEP-1998;	98US-010062P.	
PR	16-SEP-1998;	98US-010064P.	
PR	17-SEP-1998;	98US-010083P.	
PR	17-SEP-1998;	98US-010064P.	
PR	17-SEP-1998;	98US-0100710P.	

PR	10-NOV-1998;	98US-0107783P.	Query Match	100.0%;	Score 1374;	DB 7;	Length 248;
PR	17-NOV-1998;	98US-0108779P.	Best Local Similarity	100.0%;	Pred. No. 3.8e-98;		
PR	17-NOV-1998;	98US-0108787P.	Matches 248;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
PR	17-NOV-1998;	98US-0108788P.	Qy	1 MGLSIFLILCVGLSQATPKIFNGTECRNSQPMWGLFEGTSRLCGVLDHRWLTA 60			
PR	17-NOV-1998;	98US-0108801P.	Db	1 MGLSIFLILCVGLSQATPKIFNGTECRNSQPMWGLFEGTSRLCGVLDHRWLTA 60			
PR	17-NOV-1998;	98US-0108802P.	Qy	61 AHCSGRYWWLGEHSLSQDWTQEQRHSGFVTHPEYLGASTSHEDLRLLRLRLPVRV 120			
PR	17-NOV-1998;	98US-0108806P.	Db	61 AHCSGRYWWLGEHSLSQDWTQEQRHSGFVTHPEYLGASTSHEDLRLLRLRLPVRV 120			
PR	17-NOV-1998;	98US-0108807P.	Qy	121 TSSVQPLPLPDNCATAGTECHVSGKGTINHPRNPPDILQCLNLSTVSHATCHGTVYGR 180			
PR	17-NOV-1998;	98US-0108867P.	Db	121 TSSVQPLPLPDNCATAGTECHVSGKGTINHPRNPPDILQCLNLSTVSHATCHGTVYGR 180			
PR	17-NOV-1998;	98US-0108857P.	Qy	181 TSNMVCAGGGVPGQDAQGDSCGPVLYGGVQLGLVSRSVGPGQDGAPGVTTICRVWD 240			
PR	18-NOV-1998;	98US-0108838P.	Db	181 TSNMVCAGGGVPGQDAQGDSCGPVLYGGVQLGLVSRSVGPGQDGIPGVTTICRVWD 240			
PR	18-NOV-1998;	98US-0108849P.	Qy	241 IRMIMRN 248			
PR	18-NOV-1998;	98US-0108850P.	Db	241 IRMIMRN 248			
PR	18-NOV-1998;	98US-0108851P.	Qy	241 IRMIMRN 248			
PR	18-NOV-1998;	98US-0108852P.	Db	241 IRMIMRN 248			
PR	18-NOV-1998;	98US-0108858P.	Qy	241 IRMIMRN 248			
PR	18-NOV-1998;	98US-0108904P.	Db	241 IRMIMRN 248			
PR	22-DEC-1998;	98US-0113296P.	Qy	241 IRMIMRN 248			
PR	30-DEC-1998;	98US-0114223P.	Db	241 IRMIMRN 248			
PR	05-JAN-1999;	99W0-US0001016.	Qy	241 IRMIMRN 248			
PR	16-APR-1999;	99US-0129674P.	Db	241 IRMIMRN 248			
PR	23-JUN-1999;	99US-0141037P.	Qy	241 IRMIMRN 248			
PR	20-JUL-1999;	99US-01441758P.	Db	241 IRMIMRN 248			
PR	26-JUL-1999;	99US-0145638P.	Qy	241 IRMIMRN 248			
PR	01-SEP-1999;	99W0-US020111.	Db	241 IRMIMRN 248			
PR	15-SB-1999;	99W0-US021194.	Qy	241 IRMIMRN 248			
PR	29-OCT-1999;	99US-0162506P.	Db	241 IRMIMRN 248			
PR	30-NOV-1999;	99W0-US028313.	Qy	241 IRMIMRN 248			
PR	02-DEC-1999;	99W0-US028351.	Db	241 IRMIMRN 248			
PR	16-DBC-1999;	99W0-US03095.	Qy	241 IRMIMRN 248			
PR	05-JAN-2000;	2000W0-US000219.	Db	241 IRMIMRN 248			
PR	06-JAN-2000;	2000W0-US000376.	Qy	241 IRMIMRN 248			
PR	11-FBB-2000;	2000W0-US003565.	Db	241 IRMIMRN 248			
PR	18-FBB-2000;	2000W0-US004342.	Qy	241 IRMIMRN 248			
PR	24-FBB-2000;	2000W0-US005004.	Db	241 IRMIMRN 248			
PR	02-MAR-2000;	2000W0-US005841.	Qy	241 IRMIMRN 248			
PR	15-MAR-2000;	2000W0-US006884.	Db	241 IRMIMRN 248			
PR	17-MAY-2000;	2000W0-US013705.	Qy	241 IRMIMRN 248			
PR	30-MAY-2000;	2000W0-US014042.	Db	241 IRMIMRN 248			
PR	02-JUN-2000;	2000W0-US014941.	Qy	241 IRMIMRN 248			
PR	23-AUG-2000;	2000W0-US015264.	Db	241 IRMIMRN 248			
PR	24-AUG-2000;	2000W0-US023122.	Qy	241 IRMIMRN 248			
PR	08-NOV-2000;	2000W0-US030952.	Db	241 IRMIMRN 248			
PR	10-NOV-2000;	2000W0-US030973.	Qy	241 IRMIMRN 248			
PR	01-DEC-2000;	2000W0-US032678.	Db	241 IRMIMRN 248			
PR	28-FEB-2001;	2001W0-US006520.	Qy	241 IRMIMRN 248			
PR	01-MAR-2001;	2001W0-US006666.	Db	241 IRMIMRN 248			
PR	01-JUN-2001;	2001W0-US012800.	Qy	241 IRMIMRN 248			
PR	20-JUN-2001;	2001W0-US019692.	Db	241 IRMIMRN 248			
PR	29-JUN-2001;	2001W0-US021066.	Qy	241 IRMIMRN 248			
PR	09-JUL-2001;	2001W0-US021735.	Db	241 IRMIMRN 248			
PR	04-SEP-2001;	2001US-00946374.	Qy	241 IRMIMRN 248			
XX			XX				
PA	(GETH) GENENTECH INC.		XX				
XX	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Hillian KJ, Gao W, Godowski PJ, Grimaldi JC, Gurney AL, Pan J, Paoletti JP, Smith V, Stewart TA, Tumatis D, Williams PM, Wood WI, Watanabe CK, XX		PR	01-SEP-1998;	98US-0098843P.	PR	10-SEP-1998;
PT	Novel isolated PRO polypeptide, useful for treating cancerous tumors, cardiac insufficiency disorders, wound healing, diabetes mellitus, thalassemias.		PR	01-SEP-1998;	98US-0099536P.	PR	10-SEP-1998;
PT	The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity		PR	01-SEP-1998;	98US-009956P.	PR	10-SEP-1998;
PT	Claim 12; SEQ ID NO 194; 556pp; English.		PR	01-SEP-1998;	98US-009958P.	PR	10-SEP-1998;
PS	XX		PR	01-SEP-1998;	98US-0099615P.	PR	10-SEP-1998;
CC	XX		PR	01-SEP-1998;	98US-0099816P.	PR	10-SEP-1998;
CC	XX		PR	01-SEP-1998;	98US-0100385P.	PR	15-SEP-1998;
CC	XX		PR	01-SEP-1998;	98US-0100388P.	PR	15-SEP-1998;

PR	98US-0106248P.	29-OCT-1998;	98US-0106384P.	
PR	98US-0105840P.	29-OCT-1998;	98US-0106500P.	
PR	98US-0106627P.	29-OCT-1998;	98US-0106464P.	
PR	98US-0106616P.	30-OCT-1998;	98US-0106464P.	
PR	98US-0106622P.	03-NOV-1998;	98US-0106856P.	
PR	98US-0106644P.	03-NOV-1998;	98US-0106922P.	
PR	98US-0106648P.	03-NOV-1998;	98US-0106922P.	
PR	98US-0106838P.	03-NOV-1998;	98US-0106930P.	
PR	98US-0106844P.	03-NOV-1998;	98US-0106919P.	
PR	98US-0106710P.	03-NOV-1998;	98US-0106932P.	
PR	98US-0106711P.	03-NOV-1998;	98US-0106934P.	
PR	98US-0106919P.	10-NOV-1998;	98US-0107783P.	
PR	98US-0106930P.	17-NOV-1998;	98US-0108802P.	
PR	98US-0106848P.	17-NOV-1998;	98US-0108806P.	
PR	98US-0106849P.	17-NOV-1998;	98US-0108807P.	
PR	98US-0106104P.	17-NOV-1998;	98US-0108867P.	
PR	98US-0106105P.	17-NOV-1998;	98US-0108738P.	
PR	98US-0106106P.	17-NOV-1998;	98US-0108848P.	
PR	98US-01061071P.	17-NOV-1998;	98US-0108849P.	
PR	98US-01061279P.	17-NOV-1998;	98US-0108849P.	
PR	98US-01061471P.	17-NOV-1998;	98US-0108851P.	
PR	98US-01061472P.	17-NOV-1998;	98US-0108851P.	
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PR	98US-01061475P.	17-NOV-1998;	98US-0108852P.	
PR	98US-01061476P.	17-NOV-1998;	98US-0108854P.	
PR	98US-01061477P.	18-NOV-1998;	98US-0108854P.	
PR	98US-01061479P.	18-NOV-1998;	98US-0108854P.	
PR	98US-01061738P.	18-NOV-1998;	98US-0108854P.	
PR	98US-01061741P.	18-NOV-1998;	98US-0108854P.	
PR	98US-01061743P.	18-NOV-1998;	98US-0108854P.	
PR	98US-01061915P.	22-DRC-1998;	98US-0113236P.	
PR	98US-01061916P.	30-DBC-1998;	98US-0114223P.	
PR	98US-0106207P.	05-JAN-1999;	99W0-US000106.	
PR	98US-01062240P.	16-APR-1999;	99US-0129674P.	
PR	98US-01062307P.	23-JUN-1999;	99US-0141037P.	
PR	98US-01062330P.	26-JUL-1999;	99US-0144758P.	
PR	98US-01062331P.	01-SEP-1998;	99US-0145638P.	
PR	98US-01062484P.	01-SBP-1999;	99W0-US021111.	
PR	98US-01062487P.	15-SBP-1999;	99W0-US021194.	
PR	98US-01062570P.	29-OCT-1999;	99US-0162506P.	
PR	98US-01062571P.	30-NOV-1999;	99W0-US028313.	
PR	98US-01062684P.	02-DBC-1999;	99W0-US028351.	
PR	98US-01062687P.	16-DBC-1999;	99W0-US030095.	
PR	98US-01062965P.	01-SBP-1999;	99W0-US030376.	
PR	98US-01063258P.	06-JAN-2000;	2000W0-US000376.	
PR	98US-01063449P.	11-FEB-2000;	2000W0-US03565.	
PR	98US-0106314P.	18-FEB-2000;	2000W0-US04342.	
PR	98US-01063315P.	02-MAR-2000;	2000W0-US005004.	
PR	98US-01063328P.	02-MAR-2000;	2000W0-US05841.	
PR	98US-01063395P.	05-MAR-2000;	2000W0-US05841.	
PR	98US-01063401P.	06-JAN-2000;	2000W0-US023328.	
PR	98US-01063433P.	08-NOV-2000;	2000W0-US030952.	
PR	98US-01063678P.	10-NOV-2000;	2000W0-US030873.	
PR	98US-01065002P.	01-DBC-2000;	2000W0-US032678.	
PR	98US-01065104P.	02-MAR-2001;	2001W0-US006520.	
PR	98US-01065169P.	24-AUG-2000;	2000W0-US023522.	
PR	98US-01065266P.	02-JUN-2001;	2001W0-US017800.	
PR	98US-01065693P.	22-OCT-2001;	2001W0-US019992.	
PR	98US-01065694P.	26-OCT-2001;	2001W0-US021064.	
PR	98US-01065807P.	09-JUL-2001;	2001W0-US021375.	
PR	98US-01065881P.	04-SEP-2001;	2001US-00946374.	
XX			(GBTH) GENENTECH INC.	
PA			Baker KP, Botstein D, Desnoi,	
PI			Gao W, Goddard A, Godowski	
PI			Pan J, Paoni NF, Roy MA, S	
PI			Williams PM, Wood WI;	
DP			WPT: 2003-186999/74	

DR N-PSDB; ADD39308.
 XX Novel isolated PRO polypeptide useful for tissue typing, modulating
 PT biological activity of cell, as molecular weight markers in protein
 PT electrophoresis, for treating arthritis, tumor.
 XX
 .Claim 12: SEQ ID NO 194: 550pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query	MGLSIEFLILCVIGLSQATAPKILFNGTRGRNSOPWQGLFEGTSIRGGVLTIDHRAYVLTAA	Score 1374;	DB 7;	Length 248;
Best Local Similarity	100.0%;	Pred. No.	3	8e-98;
Matches	248;	Mismatches	0;	Indels 0;
Db	1 MGLSIEFLILCVIGLSQATAPKILFNGTRGRNSOPWQGLFEGTSIRGGVLTIDHRAYVLTAA	60		
Qy	61 AHSGSRVYWRVLGEHSISOLDWEQIRHSGFSYTHPGYLGASTSHEDLRLRLPVRV	120		
Db	61 AHSGSRVYWRVLGEHSISOLDWEQIRHSGFSYTHPGYLGASTSHEDLRLRLPVRV	120		
Qy	121 TSSVQPLPNDCATAGTECHYSGWGITNHPRNPFPDILQCLNLSTVSHATCHGVYFGRV	180		
Db	121 TSSVQPLPNDCATAGTECHYSGWGITNHPRNPFPDILQCLNLSTVSHATCHGVYFGRV	180		
Qy	181 TSMIVCAGGVPGQDACQSDSGGPVYCCAVLOGIVSWSVGSVGPQCGDGI PGVTTIICKYVWD	240		
Db	181 TSMIVCAGGVPGQDACQSDSGGPVYCCAVLOGIVSWSVGSVGPQCGDGI PGVTTIICKYVWD	240		
Qy	241 IRMIMRN 248			
Db	241 IRMIMRN 248			

Search completed: June 16, 2004, 15:04:50
 Job time : 63 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on June 16, 2004, 15:02:46 - Search time 21 seconds

1135.976 Million cell updates/sec
(without alignments)

Title: US-10-006-116A-194
Perfect score: 1374

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Gapop 10.0 , Gapext 0.5

searched: 283366 seqs, 96191526 residues

total number of hits satisfying chosen parameters:

maximum DB seq length: 200000000

cost-processing: Minimum Match 0%

Visited first 45 summaries

Database : DTB 7861

1: piri:^{*}

3: pir3:*

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Fig. No. 18. The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

סמסטר

Result No.	Query		Length	DB ID	Description
	Score	Match			
1	622.5	45.3	260	2	156559 neuropsin -
2	569.5	41.4	248	2	555066 trypsin (EC
3	567	41.3	248	2	555067 trypsin (EC
4	561	40.8	231	1	TRPCTR trypsin (EC
5	555	40.4	243	2	A35871 trypsin (EC
6	555	40.4	253	2	A53968 serine prote-
7	553	40.2	246	2	B25528 trypsin (EC
8	552	40.2	229	1	TRBOTR trypsin (EC
9	550	40.0	247	2	S13813 trypsin (EC
10	546	39.7	247	1	TRDG trypsin (EC
11	545	39.7	246	1	TRDSC trypsin (EC
12	544.5	39.6	247	2	A27547 trypsin (EC
13	543	39.5	248	1	TRRT1 trypsin (EC
14	540	39.5	238	2	S31779 trypsin (EC
15	532.5	38.8	247	2	S05494 trypsin (EC
16	532	38.7	246	1	TRRT2 trypsin (EC
17	527	38.4	261	2	A31136 tissue kalli-
18	524	38.1	232	1	KQPG tissue kalli-
19	50.5	37.9	261	2	A25606 tissue kalli-
20	51.9	37.8	246	2	JQ1471 trypsin (EC
21	51.8	37.7	246	2	JQ1472 trypsin (EC
22	51.8	37.7	261	2	A31079 tissue kalli-
23	513.5	37.4	231	2	S31778 tissue kalli-
24	513.5	37.4	239	2	A27207 tissue kalli-
25	511.5	37.2	261	2	S45303 tissue kalli-
26	510.5	37.2	261	2	NGMSG 76 nerve gr-
27	50.8	37.0	261	1	NGMSG trypsin (EC
28	50.8	37.0	242	2	S31775 trypsin (EC
29	50.8	37.0	242	2	S31776 trypsin (EC

APPENDICES

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RESULT 2
S55066          trypsin (BC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken
N;Alternate names: trypsinogen II
C;Species: Gallus gallus (chicken)
C;Date: 23-Aug-1995 #Sequence_revision 19-Oct-1995 #text_change 22-Jun-1999
C;Accession: S55066; S72347

Db          133 GDIKVVKPQLANLCPKPVQKCIIISGKWTIVTISPOINPPTNLCAEYKIVYSQNKCERAYPGKIKI 191
Db          181 TSNMVCAAGGVPCQDACA CGDSCGSPVLCGVLVCGVTVGLQLYSWGPGCGDQGIPSTVYTIKAKYVDW 240
Qy          193 TEGMVCAAGSSNEADTCQGDSCGSPVLCGDMGQITSGWS-DPCGRPBKGVTICRYTTW 251
Db          241 IRRIMRN 247
Qy          252 IKKTMDDN 258

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P;60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.8%; Score 561; DB 1; Length 231;
Best Local Similarity 46.7%; Pred. No. 1; e-38;
Matches 107; Conservative 39; Mismatches 77; Indels 6; Gaps 4;

Qy 21 KIFNGTECCRNISQPVQHPEGTSLRCCGLIDHRWLTAAHGSRSRYTWRLGEHSLSQL 80
Db 8 KTVGGYCTRANS1PQVSNLSSHF--CCGLINSQWVSAACYKSR1QVRLEHENNDVL 66

Qy 81 DWTEQIRHSGPSVTHPQTGASTSHEHDRLRLRPLPRVTSSQPLPLPNDCATAGTC 140
Db 67 EGNEQFNAKITHPNFG--NTLNDIMLIKLSSPATLNSRVATSLPSRCAAGTC 124

Qy 141 HVSGWGIITNTHRAFPDQLQCLNLISIVSHTATCHGVYPERITSNNMVCAGGP-GDAGCGD 199
Db 125 LISGWGNTKSSGSSYPSLQCLKAPVLSISSCKSYSPGTENMICVPLERGSDSCGD 184

Qy 200 SGSPLVCGGVLQGYVSKGSSVGPCQDGTPGIVTYICKYDWRMIMANN 248
Db 185 SGGEVVNCNQLOGIYVSKY--GCAQKRNKGVYKVCVNVWICOTIAN 231

RESULT 5

A35871 trypsin (BC 3.4.21.4) precursor, pancreatic - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 04-Mar-2000
C:Accession: A35871; S12117
R: Shi, Y.B.; Brown, D.D.
Genes Dev. 4, 1107-1113, 1990
A;Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes in X
A;Reference number: A35871; MUID: 91007255; PMID: 2210372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243 <SH1>
A;Cross-references: ENBLL:X53458; PIDN:CAA37538.1; PID:965163
C;Keywords: hydrolyase, protein digestion, serine proteinase
F;1-15/Domain: signal sequence #status predicted <SIG>
F;21-236/Domain: activation peptide #status predicted <APT>
F;26-243/Product: trypsin I #status predicted <MAT>
P;60,104,197/Active site: His, Asp, Ser #status predicted

Query Match 40.4%; Score 555; DB 2; Length 243;
Best Local Similarity 45.7%; Pred. No. 4; e-38;
Matches 113; Conservative 42; Mismatches 82; Indels 10; Gaps 6;

Qy 6 PFLJCVLGLSQAT---PKIENGTGCRNISQPVQHGFEGTSURCGSVLIDHRWLTAAH 62
Db 3 PFLJCVL-LGAALAFDDKIGGATCAKSVPVTLNSYHF-CGGSLLTQNQWVSAAH 60

Qy 63 CCGSRYWVLRGEHSLSQLDWTQIRHSGFSTWPHLGASTSHEDRLRLRPLPYRTS 122
Db 61 CYKASIQVRLGEHNIALSFTGTFISSSKVTRISGY--NSVTLNDNDMLIKLSSPASINA 118

Qy 123 SVOPPLPNDCATAGTGCVSGRGTINHPRNPFPDLLOCLNLSIVSHTACHGVYGRITS 182
Db 119 AVTVPLPQGCCAGTSCSLLSGNTLNSGNTSPDLQCLNAPLTLRQNCAYPGFETIA 178

Qy 183 NMICAGGVP-GDAGCGDGGP1NYC6GVLQGNYWSGSVGPQCGDGIPEVYTYICKYDVI 241
Db 179 NMICAGGVPMEGGDKSDGGPQVNGQ1QGvVSWG1--GCAMRNPVSYTCNTNAWI 236

Qy 242 RMIMANN 248
Db 237 QNTIAAN 243

RESULT 6

A53968 serine proteinase SCCB precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C:Accession: A53968
R:Hansson, L.; Stromqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Bgelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enyz
A;Reference number: A53968; MUID: 94308225; PMID: 8034709
A;Accession: A53968
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
C:Genetic:
A;Cross-references: GB:L33404; NID:9521214; PIDN: AAC37551.1; PID:g332504
A;Gene: GDB:PRSS6; SCCB
A;Cross-references: GDB:377730
A;Map position: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>

Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.6%; Pred. No. 4; e-38;
Matches 115; Conservative 37; Mismatches 90; Indels 16; Gaps 6;

Qy 1 MGTSIPLLICVIGLS-----QATTPKIFNGTECRNSOPMOVGLPDTSTLRCGGVLI 52
Db 1 MARSLLPLQIILSLALISTAGEAQQDRIIDAPCARGSHMQLVALSGNOLHQGGVVL 60

Qy 53 DHRWLTAAHCSGSRYWVLRGEHSLSQLDWTQIRHSGFSVTWPHLGASTSHEDRLRL 112
Db 61 NERWVLTAAHCKRNKETYTHLGSPTLG--DRRAQRKASKSFRHPG--STOTHNDLMVV 116

Qy 113 RULPVRUTSSVPLPLENDCATAGTGCVSGRGTINHPRNPFPDLLOCLNLSIVSHTAC 172
Db 117 KLNQSARLSSMYKVKRLPSRCBEPGTTCTVSGKGTTSVDVTPSPDLCYDKLSPQDC 176

Qy 173 HGVYPGRITSNNVYCAAGGVPG--QDAACQDSGGPLVCGAVLQGIVVSWSVGPCCGDIQPGV 230
Db 177 TKYKQDLSLBNSMUCA-GTPDSKKNACNEDSGGDLVCRGTLQGLVSWGTF-PCGGPNDPGV 234

Qy 231 YTVICKYWDWIRMIMANN 248
Db 235 YTVCKEFTKWNIDTMKCH 252

RESULT 7

B25528 trypsin (BC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A;Title: Sequence organisation and transcriptional regulation of the mouse elastase II .
A;Reference number: A93646; MUID: 87066713; PMID:364189
A;Accession: B25528
A;Molecule type: mRNA
A;Residues: 1-246 <STB>
A;Cross-references: GB:X04574; NID:954918; PIDN:CAA28243.1; PID:g54919
C;Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; protein sequence #status predicted <MAT>
P;1-23/Domain: signal sequence predicted <TRY>
P;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
P;63,107,200/Active site: His, Asp, Ser #status predicted
P;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.2%; Score 553; DB 2; Length 246;
Best Local Similarity 44.7%; Pred. No. 6; e-38;
Matches 113; Conservative 45; Mismatches 81; Indels 14; Gaps 7;

Qy	3 LSTIPLLCVIGLSQ---ATPKIENGTBCGRNSPWWOVELFEGTSRRCGGVLIDHFWLTAAHCSSRYWTLGEHSILSQL 58
Db	1 MSALLALVALGAAVAPPVDDDKIVGGTCRESSPPYQISLNAGTHP-CGGSILNDQWTV 59
Qy	59 TAAHCGSGSRVWRLLGEHSLSDWTEQIRHSGFGSFYTHPGTIGASTSHEHDILRLRLRLRPLV 118
Db	60 SAARCYKTRIQVRUGEBHNIVLEGQFQVDASAKIRHPTN-NSFLDNDIMLKLASPV 117
Qy	119 RVTSSQPLPLENDCATAGTCHEVYSGWG---ITNHPRNPFPDLQLCINLSTIVSHANCHGVY 176
Db	118 TLNARAVSYBLPSSCAPAGTOCLISGWNTLNSNGTNN---PDLLQCYDAPIVPOAECASY 175
Qy	177 PGRITSNMVYCAAGVPE-GDACAQGDGGPLVCGGVVQGLYNSWGSVPGPQGDGIPGTYTIC 235
Db	176 PGDITNNMVCVGLLEGGDKSCQDGSPVYNGBLOVIVSWGY-GCAQPDAPGTYTKVC 233
Qy	236 KVDWIRMMRNN 248
Db	234 NYVDWIQNTIADN 246
RESULT 8	
trypsin (EC 3.4.21.4) precursor - bovine	
N; Contains: trypsinogen	
C; Species: Bos primigenius taurinus (cattle)	
C; Date: 24-Apr-1984 #sequence revision 28-Feb-1986 #text_change 18-Jul-1997	
C; Accession: A90164; A00946; S08774	
R; Mikes, O.; Holleysovy, V.; Tomasek, V.; Sorm, F.	
Biochem. Biophys. Res. Commun. 14, 346-352, 1966	
A; Title: Covalent structure of bovine trypsinogen. The position of the remaining amides.	
A; Reference number: A90164; MUID:67168848; PMID:5967094	
A; Accession: A90164	
A; Molecule type: protein	
A; Residues: 1-57, 'Q', '59-67, 'Q', '69-150, 'N', '152-176, 'N', '178-229 <MIK>	
R; Hartley, B.S.	
Philos. Trans. R. Soc. Lond. B257, 77-87, 1970	
A; Reference number: A93755	
A; Contents: annotation; revisions	
R; Titani, K.; Bricebon, L.H.; Neurath, H.; Walsh, K.A.	
Biochemistry 14, 1358-1366, 1975	
A; Title: Amino acid sequence of dogfish trypsin.	
A; Reference number: A00950; MUID:5146645; PMID:1092332	
A; Contents: annotation; revisions	
A; Note: the sequence agrees with that shown	
R; Bode, J.; Schwager, P.	
J. Mol. Biol. 98, 693-717, 1975	
A; Title: The refined crystal structure of bovine beta-trypsin at 1.8 angstrom resolution	
A; Reference number: A93954; MUID:7607297; PMID:512	
A; Contents: annotation; X-ray crystallography; binding sites for calcium, substrate, and	
C; Comment: Trypsinogen is synthesized in the acinar cells of the pancreas	
C; Comment: Autocatalytic cleavage after Lys-6 leads to beta-trypsin by releasing a terminal pseudotrypsin. A cleavage may also occur after Arg-105.	
C; Superfamily: trypsin; trypsin homology	
C; Keywords: hydroase; pancreas; protein digestion; serine proteinases; zymogen	
P-1-229/Product: trypsinogen #status experimental <ZM>	
P-1-6/Domain: trypsin homology <TRY>	
P-7-222/Domain: trypsin homology <APY>	
P-6-7/Cleavage site: Lys-1-ile (enteropeptidase) #status experimental	
P-6-7/Cleavage site: Lys-229-229/Product: alpha-trypsin #status experimental <MPF>	
P-13-133/Domain: trypsin homology <TRY>	
P-13-133,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: #status experimental	
P-46,90-183/Active site: His, Asp, Ser #status experimental	
P-58,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) #status experimental	
P-131-132/Cleavage site: Lys-Ser (autolytic) #status experimental	
Query Match 40.2% Score 552: DB 1: Length 229;	
Best Local Similarity 46.3%; Pred. No. 7.1e 38;	
Matches 106; Conservative 40; Mismatches 77; Indels 6; Gaps 4;	
Qy	21 KIFNGTECCRNSQSPWQVGLFEGTSRRCGGVLIDHFWLTAAHCSSRYWTLGEHSILSQL 80
Db	6 KIVGGTYCTTCATGTTTTCYQVSUNSGYRP-CGGSILNDQWTVSAHCFSGIOVRLGENTYI 64

Qy	81	DWTBQIRHSGFSVTQHCGAATLRLRPLPVRTTSVQLPLPNDCATGTEC	140
	:	: : : : : : :	
Db	65	EGNEQTISASXIVHESY - NSNTLNDIMILKASASLNSRVASISLSPSCASGTQC	122
Qy	141	HVSGRGTTNHPRNPDPDLOCLNLSTVSHATCHGTVYGRITISNMYCAGGYP - GODACQGD	199
	: : : : : : : : : : :		
Db	123	LISGWRNTKSSTGTSYDVKLCKAPLSDSSCKSAPQQTISNMPCAGYLEGGKDSQGD	182
Qy	200	SGGPLIQCQGVHQGLQGLWNGSVCPGQDGIPGTVTYTICKYDWMIRMMRN	248
	: : : : : : : : : : :		
Db	183	SGGPVYCSGKLGQIVNGS - GCAQAKPGTVYKVNYYSWIKQTIAASN	229
RESULT 9			
Qy	S13813	trypsin (BC 3.4.21.4) - bovine	
	C;Species: Bos Primigenius taurinus (cattle)		
	C;Accession: S13813		
	C;Date: 02-Dec-1993 #text_change 03-Aug-1995 #text_change 22-Jun-1999		
	R;le Ruerou, I.; Guilloteau, P.; Touillec, R.; Puigserver, A.		
	R;J. Biochem. 193, 767-773, 1990		
	A;Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic a		
	A;Reference number: S13813; PMID:9065383; PMID:1701147		
	A;Accession: S13813		
	A;Status: preliminary		
	A;Molecule type: mRNA		
	A;Residues: 1-247 _C		
	A;Cross-references: EMBL:X54703; NID:g929; PIDN:CPA38513.1; PID:9830		
	C;Superfamily: trypsin; trypsin homology		
	C;Keywords: hydrolase; protein digestion; serine proteinase		
	F;24-239/Domain: trypsin homology <TRY>		
	F;63-107/200/Active site: His, Asp, Ser #status Predicted		
Query	40.0t	Score 550; DB 2; Length 247;	
Best Local Match	45.7%	Pred. No. 1.1e-37;	
Matches	113;	Conservative 40; Mismatches 84;	
		Indels 10; Gaps 5;	
Qy	7	LILCVLGLSQ---ATPKIENGTCTEGRNSOPWQVSLFEGTSLRCCGVLLDHRWVLTAAH	62
	: : : : : : : :		
Db	5	LILAFGGAAYAAPPDDDKVGGTCAENSTPYQUSLNAGYHP - CGGSLLNDQWVSAAH	63
Qy	63	CGSRSRYWYRLGHHSLSQLDNTWETQIRHSGGPSTVTHPKVTLGASTSHRENDLRLRLRPLPVRTS	122
	: : : : : : :		
Db	64	CTQYHIVQLRGYNNIVDYLEGGEQFIASKCIRHPK --SSWTDNIDILLKLSTPAVINA	121
Qy	123	SYQPQLPNDATAGTCRCSNGGNTINHPRNPFDLLOCNLNSIVSATCHGVYPRITS	182
	: : : : : : : :		
Db	122	RVSTLJLPSACGACTCCLSEGMENTLSSCNYPDILQOLIVAPUJSHADCEASYPQIRNT	181
Qy	183	NMVCAAGGVP - GODACCGDSSGSPPLVCGVLLQGLVLVSRSVGPQCDGIPGVTYIICKYVDWI	241
	: : : : : : : :		
Db	182	NM1CAAGBLGGKDSCQDGGPVAQNGQLOQIVSMTY - GCAQKGPKVYTKVCNVYDVI	239
Qy	242	RMIIMRN	248
	:		
Db	240	QETIAAN	246
RESULT 10			
TRDG	trypsin (BC 3.4.21.4) precursor, anionic - dog		
	N;Alternate names: cationic trypsinogen		
	C;Species: Canis lupus familiaris (dog)		
	C;Date: 30-Sep-1997 #sequence_revision 30-Sep-1997 #text_change 18-Jun-1999		
	R;Pinsky, S.D.; LaPorre, K.S.; Scheele, G.		
	Mol. Cell. Biol. 5, 2669-2676, 1985		
	A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA		
	A;Reference number: A26273; PMID:9628462; PMID:3841794		
	A;Accession: A26273		
	A;Molecule type: mRNA		
	A;Residues: 1-247 _C		

A;Cross-references: GB:M11589; NID:gi164094; PID:AAA30899.1; PID:gi164095 C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen P;1-15/Domain: signal sequence #status predicted <SIG> P;16-23/Domain: activation peptide #status predicted <APT> P;24-247/Product: trypsin; anionic #status predicted <ENZ> P;24-239/Domain: trypsin homology <TRY> P;30-160,48-54,132-233,139-206,171-185/Disulfide bonds: #status predicted P;73,107,200/Active site: His, Asp, Ser #status predicted P;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted	Query Match 39.7%; Score 546; DB 1; Length 247; Best Local Similarity 45.6%; Pred. No. 2.4e-37; Matches 113; Conservative 38; Mismatches 85; Indels 12; Gaps 6;	Qy 119 RVTSSVOPPLPNDCATAGTCVSGITNHPNPPDLOCLNLIVSHATCHGVYPG 178 Db 118 TLNSRVSAAALPKSCPAAGTQCLISGWATQSIGGNYPDVLQCLMAPILSDSVCNAYPG 177
Qy 7 LILICVGLSQANTP ---KIRNGTECGGANSQPOVQGLPEGTSLRCGGVLLIDRKWLTAA 61 Db 5 LILLAFLG- AAVATPTDDDDLKVGGTYCTCBENSVPQVSUNAGYHF-CGSSLISDOWVSA 62	Qy 179 RITSNNYCAAGGVP-GODACQGDSCGSPLYCGSVPWGLVSGVTPGQDGPQG 237 Db 178 QISSNNMIGYMEGGEDKSCGDSEPPVNGEGLQGVVNSGA--GCAQKGKPGVSSRVCKY 235	Qy 119 RVTSSVOPPLPNDCATAGTCVSGITNHPNPPDLOCLNLIVSHATCHGVYPG 178 Db 118 TLNSRVSAAALPKSCPAAGTQCLISGWATQSIGGNYPDVLQCLMAPILSDSVCNAYPG 177
Qy 62 HCGSGRYWWRGEHSLSQLDWTBQIIRHSEPSVTHFGYLGASTSHEHDRLRLRPLPVRT 121 Db 63 HCYSRRIQRQLGENINIDLEGENEFINSAKVIRHNPY -NSWLNDNDLKLKSSPAVN 120	Qy 122 SSVQPLPNDCATAGTCVSGITNHPNPPDLOCLNLIVSHATCHGVYPG 181 Db 123 ARVATISPRACAAGFTQCLISGNGNTLGSNTYPELQCLADPLTQOQCRASYPGQT 180	Qy 179 RITSNNYCAAGGVP-GODACQGDSCGSPLYCGSVPWGLVSGVTPGQDGPQG 237 Db 178 QISSNNMIGYMEGGEDKSCGDSEPPVNGEGLQGVVNSGA--GCAQKGKPGVSSRVCKY 235
Qy 182 SNNYCAGGVP-GODACQGDSCGSPLYCGSVPWGLVSGVTPGQDGPQG 240 Db 181 ENMICAGPFLLEGKRDSCGSGGPVVCNGSLSQGIVSWGY--GCAQKRNKEPVYKWCNPFVNW 238	Qy 241 IRMMRNN 248 Db 239 IQSTIAAN 246	Qy 119 RVTSSVOPPLPNDCATAGTCVSGITNHPNPPDLOCLNLIVSHATCHGVYPG 178 Db 118 ATLNRSRVSTVSLPSSGSSCTKLVSGKNTLSSGNTNYSLSQCLADPVLSDSCKSSSY 177
Qy 241 IRMMRNN 248 Db 239 IQSTIAAN 246	Qy 3 LSIPHLLCVGLGLSQA-----TPKIFNGTECGRNSQPOVQGLPEGTSLRGCGVLDHRYV 57 Db 1 MKRLPLFAFGAAVLPDQDDDKVGGTTCQNSLSPYQVSUNAGYHF-CGSSLISQWV 59	Qy 178 GRITSNNYCAAGGVP-GODACQGDSCGSPLYCGSVPWGLVSGVTPGQDGPQG 236 Db 178 GKITSSNMPFLGFLBQGKSDQGNSGPVVNGQDGVVNSGY--GCAQKGKPGVITKVCN 235
RESULT 11 TRYDC trypsin (EC 3.4.21.4) precursor, cationic - dog	N;Alternate names: cationic trypsinogen C;Species: Canis lupus familiaris (dog) C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999 C;Accession: B26273 R;pinsky, S.D.; Laforge, K.S.; Scheele, G. Mol. Cell. Biol. 5, 2659-2676, 1985 A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequence A;Reference number: A26273; PMID:86284628; A;Molecule type: mRNA A;Residues: 1-246 <PIN> C;Superfamily: trypsin; trypsin homology C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen P;1-15/Domain: signal sequence #status predicted <SIG> P;22-246/Product: trypsin; cationic #status predicted <ENZ> P;24-239/Domain: trypsin homology <TRY> P;30-160,48-54,132-233,139-206,171-185/Disulfide bonds: #status predicted P;63,107,200/Active site: His, Asp, Ser #status predicted P;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted	Qy 3 LSIPHLLCVGLGLSQA-----TPKIFNGTECGRNSQPOVQGLPEGTSLRGCGVLDHRYV 57 Db 1 MKRLPLFAFGAAVLPDQDDDKVGGTTCQNSLSPYQVSUNAGYHF-CGSSLISQWV 59
Qy 39.7%; Score 545; DB 1; Length 246; Best Local Similarity 44.2%; Pred. No. 2.9e-37; Matches 111; Conservative 43; Mismatches 87; Indels 10; Gaps 6;	Qy 3 LSIPHLLCVGLGLSQA-----ATPKIFNGTECGRNSQPOVQGLPEGTSLRGCGVLDHRYV 58 Db 1 MKRLPLFAFGAAVLPDQDDDKVGGTTCQNSLSPYQVSUNAGYHF-CGSSLISQWV 59	Qy 39.7%; Score 545; DB 1; Length 246; Best Local Similarity 44.2%; Pred. No. 2.9e-37; Matches 111; Conservative 43; Mismatches 87; Indels 10; Gaps 6;
Qy 59 TAARHSGSRWWRGEHSLSQLDWEQIRHSEPSVTHFGYLGASTSHEHDRLRLRPLPVRT 118 Db 60 SAAHCYKSRRIQVRGEYNIAVSEGEQFNAAKTRHPPY-NANTIDIMLKLSSSA 117	Qy 59 TAARHSGSRWWRGEHSLSQLDWEQIRHSEPSVTHFGYLGASTSHEHDRLRLRPLPVRT 118 Db 60 SAAHCYKSRRIQVRGEYNIAVSEGEQFNAAKTRHPPY-NANTIDIMLKLSSSA 117	Qy 237 YDWMRMRNN 248 Db 236 YVNTIQQTAAAN 247
RESULT 13 TRYTRI trypsin (EC 3.4.21.4) I precursor - rat	N;Alternate names: trypsinogen I C;Species: Rattus norvegicus (Norway rat) C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 24-Sep-1999 C;Accession: B22657; A00948 R;Crail, C.S.; Choi, Q.I.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J. J. Biol. Chem. 259, 14255-14264, 1984 A;Title: Structure of two related rat pancreatic trypsin genes. A;Reference number: A22657; PMID:85054880; PMID:6094547 A;Molecule type: DNA A;Residues: 1-246 <CR>	Qy 237 YDWMRMRNN 248 Db 236 YVNTIQQTAAAN 247

A;Cross-references: GB:J00778; NID:9206507; PIDN:AAA98518.1; PID:g206508						
A;Note: the authors translated the codon Acr for residue 6 as Leu and GAC for residue 1						
R; MacDonald, R.J.; Starry, S.J.; Swift, G.H.						
J. Biol. Chem. 257, 9724-9732, 1982						
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of						
A;Reference number: MUID:8226524; PMID:6896710						
A;Accession: A00948						
A;Molecule type: mRNA						
A;Residues: 1-246 <MRC>						
A;Cross-references: GB:J00778; NID:9206507; PIDN:AAA98518.1; PID:g206508						
C;Superfamily: trypsin; trypsin homology						
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen						
P;1-15/Domain: signal sequence #status predicted <SIG>						
P;16-23/Domain: activation peptide #status predicted <APT>						
P;24-246/Domain: trypsin homology <TRY>						
P;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted						
P;53,107-200/Active site: His, Asp, Ser #status predicted						
P;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted						
Query Match Score 543; DB 1; Length 246;						
Best Local Similarity 44.5%; Pred. No. 4_1e-37; Indels 14; Gaps 7;						
Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;						
Qy 3 LSIFLLCVGLGSA---ATPKLFGNGTGRGRNSQPKWQVGLFLPEGTSLRGCGVVLIDHRKVL 58						
Db 1 MSAILALVALGAAVAFPLLEDDDDICVGGGTCPEHSPVYQVSLSNSXHF-CGGSLINDIQKV 59						
Qy 59 TAHCSGSRYWVRLGEHSLSQLDTEQIRHSGFSVTHPQLGASTSHEEDLRLRLRIPV 118						
Db 60 SAHACYKSRRIQVRQHNVNLVEGLDQEFINAAKIKHPNN-SSWTNLNDIMLKLSSPV 117						
Qy 119 RVTSVQVPLPLPNCATAGTCVHSGWKG--ITNHPRNPFPDLLOCNLISVSHATCHGVV 176						
Db 118 KMRARVAPVPLPACAPAOCLISGWNTLNSGVNN-PDLIUCDAPVLSQDCRAY 175						
Qy 177 PRGITSNMYCAGCTVP-GDADACQEDSGSGPGLVYCGVLYQGLYWSGSVGPCCGODGIPSVYTIC 235						
Db 176 PRGETSSMCVGPFLLEGKQDSQGDGIPVVCNGQOLQGTVWSGVY--GCALPDNPNSPVYTKVC 233						
Qy 236 KYTDWIR 242						
Db 234 NPFWIQ 240						
RESULT 14						
S31779 trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (Fragment)						
C;Species: Salmo salar (Atlantic salmon)						
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999						
C;Accession: S66657; S31779						
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Db	15	KIVGGYBCEKNSASWQASLQSGYHP-CGGSLISSTWVSAAHCYKSRIQVRGEHNIAVN	73
Qy	81	DWTEQIRHESGFSTWPGYLCASTSHEDLRLRLRPLRVTTSYQPLPLNDCATAGTCB	140
Db	74	BGTGPFDISVVKHPSY -NSRNLNDNDMLIKLRSKPASNLYSTVALPSSCASSGTRC	131
Qy	141	HVSGGITHNHPRNPPDILQCLNLSIVSHATCHGVYPRGRITSNNMVCAGGVP-GODACQGD	199
Db	132	LvsGRGNLGSSSSNTPDTLRLCDLPLTSSSCRSNSAYPGQITSNMFCAGMEGGKDSQCQD	191
Qy	200	SGGPVLVGTVYQLOGLVSWGQVGPCCQDGIFGVVYICKTVWDWIRMIAMRN	248
Db	192	SGGPVNVICNGQLOGVVSWGY - GCAQRNKEGVVTKVNCYRSWISSTMSSN	238
RESULT 15			
Qy	S05494	trypsin (EC 3.4.21.4) IV precursor - rat	
C;Species:	Rattus norvegicus (Norway rat)		
C;Accession:	005494	#sequence_revision	07-Jun-1990 #text_change 22-Jun-1999
R;Luettcke, H.; Rauch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.			
Nucleic Acids Res. 17, 6736, 1989			
A;Title:	A fourth trypsinogen (P23) in the rat pancreas induced by CCK.		
A;Reference number:	S05494	MUID:89386010; PMID:2780302	
A;Accession:	S05494		
A;Molecular type:	mRNA		
A;Residues:	I-247 <LUB>		
A;Cross-references:	EMBL:X15679; PIDN:CAA33718.1; PID:956814		
C;Superfamily:	trypsin; trypsin homology		
C;Keywords:	calcium binding; hydrolase; protein digestion; serine proteinase; z-		
C;Sequence:	proteinase; status predicted <SIC>		
P;1-15/Domain:	signal sequence #status predicted <APR>		
P;2-247/Product:	trypsin IV #status predicted <MAT>		
P;24-240/Domain:	trypsin homology <TRY>		
P;30-161	#status predicted		
P;64-108/201/Active site:	His, Asp, Ser #status predicted		
P;76,78,81,86/Binding site:	calcium (Glu, Asn, Val, Glu) #status predicted		
Query Match	38.9%	Score 533.5 ; DB 2 ; Length 247;	
Best Local Similarity	43.4%	Pred. No. 2-Se-36;	
Matches	109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;		
Qy	1	MGLSSP--LILCVLGQLSQAATPFLKIFNGTCGNSQPMWQGLPESTSRLRGVILIDHRWVL	58
Db	1	MKISFFAFLGAVALPYNDDDKVKGITCPKHLVPKYQVSLHDQISHQCGGLSISDQWVL	60
Qy	59	TAAHCSGRYVWRUGHSLSQDWTQEIRHSGFSVTHPCYLGASTSHEHDLRLRLRLRLPV	118
Db	61	SAAHYKRLQVRLGEENHVLRGEQFDARKIRHPSY--NKDTLDNDIMILKLKSPA	118
Qy	119	RVTSSVQPLPLNDCATGTECHYSGKGTNHFRNPFPDLOCLNLSIVSHATCHGVYCG	178
Db	119	VLNQGVSRTSLPRECASTDQCLVSGMNTVSIGGGKYPALLQCLBAPVTLASSCKSKYSG	178
Qy	179	RITSMVCAAGGVP-GODACQGDSEGPFLVGGVQLGVNGSVGPQDGIPGVVYICKY	237
Db	179	QITSMFCDGFLBEGKDSDGSGPVVNGRIGQIVSMGSV-CAMRKPKGTVTKVCNV	236
Qy	238	VDWIRMIAMRN	248
Db	237	LSPWQETMANN	247

Scoring table:	BLOSUM62	Gapext 10.0 , Gapext 0.5			
Searched:	141681 seqs.	52070155 residues			
Total number of hits satisfying chosen parameters:	141681				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
Database :	SwissProt_42::*	Listing first 45 summaries			
Result No.	Score	Query Match Length DB ID	Description		
1	1374	100.0 KLKC_HUMAN	Q9ukr0 homo sapien		
2	630.5	45.9 KLKB_HUMAN	Q60259 homo sapien		
3	622.5	45.3 NRPN_MOUSE	Q61195 mus musculus		
4	621.5	45.2 NRPN_RAT	Q87780 rattus norvegicus		
5	618.5	45.0 KLKB_HUMAN	Q9abx7 homo sapien		
6	599.9	43.6 KLKF_HUMAN	Q91225 homo sapien		
7	569.5	41.4 TRY3_CHICK	Q9u629 gallus gallus		
8	569.5	41.4 KLKB_HUMAN	Q9z093 homo sapien		
9	568.5	41.4 KLKC_HUMAN	Q9ukr9 homo sapien		
10	567	41.3 KLKD_HUMAN	Q9akr3 homo sapien		
11	566	41.2 TRY2_CHICK	Q9u628 gallus gallus		
12	564.5	41.1 TRY1_CHICK	Q9u627 gallus gallus		
13	564.5	41.1 KLKS_HUMAN	Q9y737 homo sapien		
14	564	41.0 KLKA_HUMAN	Q43240 homo sapien		
15	563	41.0 TRY2_XENLA	P70559 xenopus laevis		
16	561	40.8 TRY_PIG	P00761 sus scrofa		
17	561	40.8 TRY_BOVIN	P00760 bos taurus		
18	551	40.8 KLKG_HUMAN	Q9k286 homo sapien		
19	555	40.4 TRY1_XENLA	P17799 xenopus laevis		
20	555	40.4 TRY2_MOUSE	P19862 homo sapien		
21	553	40.2 TRY2_BOVIN	P01146 bos taurus		
22	550	40.0 TRY2_BOVIN	Q29463 bos taurus		
23	546	39.7 TRY2_CANFIA	P05872 canis familiaris		
24	545	39.7 TRY1_CANFIA	P06871 canis familiaris		
25	544.5	39.6 TRY3_RAT	P08426 rattus norvegicus		
26	543	39.5 TRY1_RAT	P00762 rattus norvegicus		
27	540	39.3 TRY3_SALSA	P35033 salmo salar		
28	533.5	38.8 TRY4_RAT	P12788 rattus norvegicus		
29	521.5	38.4 TRY2_RAT	P00763 rattus norvegicus		
30	521.5	38.4 KLKT_RAT	P35373 rattus norvegicus		
31	521.5	38.0 KLK_PIG	P00752 sus scrofa		
32	521.5	38.0 KLKE_MOUSE	P15947 mus musculus		
33	519	37.8 TRYA_RAT	P32821 rattus norvegicus		

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RESULT 2	
KLKB_HUMAN	STANDARD; PRT; 260 AA.
ID KLKB_HUMAN	STANDARD; PRT; 260 AA.
AC 060259; OHCBC3; Q9UQ9; Q9UQ9;	PRT; 260 AA.
DT 15-JUL-1999 (Rel. 38, Created)	
DT 15-JUL-1999 (Rel. 38, Last sequence update)	
DT 15-MAR-2004 (Rel. 43, Last annotation update)	
DT Neurosin Precursor (BC 3.4.21-1) (NP) "Kallikrein 8" (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14 protein).	
DB PRSS19 OR PRSS19 OR NRPN.	
DR KLKB_HUMAN	
DR Homo sapiens (Human).	
DR Buteleostomi; Craniata; Chordata; Mammalia; Metazoa; Primates; Eutheria; Hominidae; Homo.	
DR NCBI Taxid:9606;	
DR TAXID:9606;	
RN [1]	SEQUENCE FROM N.A. (ISOFORM 1).
RP	
RC	SEQUENCE FROM N.A. (ISOFORM 1 AND 2).
DR TISSUE=Hippocampus;	
DR MEDLINE=98372070; PubMed=9714609;	
DR Yoshihda S., Taniguchi M., Hirata A., Shiosaka S.; "Sequence analysis and expression of human neutropsin cDNA and gene.";	
DR Mitsuji S., Tsurioka N., Yamashiro K., Nakazato H., Yamaguchi N.; "A novel form of human neutropin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain.";	
DR InterPro; IPR001314; Peptidase_S1A.	
DR Pfam; PF00089; trypsin_1.	
DR PRINTS; PR0722; CHYMOTRYPSIN.	
DR PROSITE; SM00020; TRYD_SPC_1.	
DR PROSITE; PS500240; TRYPSIN_DOM_1.	
DR PROSITE; PS00134; TRYPSIN_HIS_1.	
DR PROSITE; PS00135; TRYPSIN_SER_1.	
KW Hydrolase; Serine protease; Glycoprotein; Signal; Alternative splicing.	
PT SIGNAL 1 17 KALLIKREIN 12.	POTENTIAL.
PT CHAIN 18 248 KALLIKREIN 12.	CHARGE RELAY SYSTEM (BY SIMILARITY).
PT ACT SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).	CHARGE RELAY SYSTEM (BY SIMILARITY).
PT ACT SITE 108 108 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 200 200 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 28 161 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 47 63 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 133 235 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 140 206 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 172 186 BY SIMILARITY.	BY SIMILARITY.
PT DISULFID 196 222 N-LINKED (GLCNAC. . .) (POTENTIAL).	N-LINKED (GLCNAC. . .) (POTENTIAL).
PT CARBONYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).	N-LINKED (GLCNAC. . .) (POTENTIAL).
PT CARBONYD 163 163 KYVDWTRMIMRN > NSTLVGLTSWNFNSCQPF (in isoform 2).	KYVDWTRMIMRN > NSTLVGLTSWNFNSCQPF (in isoform 2).
PT PTID=S005403.	/PTID=S005403.
SQ SEQUENCE 248 AA; 26733 MW; BB473E98FBBAFT03 CRC64;	
Query Match 100.0%; Score 1374; DB 1; Length 248;	
Best Local Similarity 100.0%; Pred. No. 1.7e-105;	
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Qy 1 MGLSIFLFLVIGLSQATPKLFLNGTECGRNSQPMQVGLPFGTSLRCGGVLDIDHWVLTAA 60	
Db 1 MGLSIFLFLVIGLSQATPKLFLNGTECGRNSQPMQVGLPFGTSLRCGGVLDIDHWVLTAA 60	
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RP MBDLINE=20510030; PubMed=11054574;	
RA Gan L., Lee I., Smith R., Wang K., McCuaig J.,	
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,	
RA Danganan L., Brier A., Christensen M., Georgescu A., Avila J., Liu S.,	
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,	
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RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,	
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RA Lamerdin J.B., McCready P.M., Skowronski E., Viswanathan V.,	
RA Burkhardt-Schulte K., Gordon L., Davis J., Davis J.,	
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,	
RA Danganan L., Brier A., Christensen M., Georgescu A., Avila J., Liu S.,	
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RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,	
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,	
RA Olsen A.S., Carrano A.V.,	
RA "Sequence analysis of chromosome 19q13.4.";	
RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.	
CC -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity.	
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.	
CC -1- SUBCELLULAR LOCATION: Secreted.	
CC -1- ALTERNATIVE PRODUCTS: Event-Alternative splicing; Named isoforms=2; Name=1;	
CC	

CC	Name=2;	Sequence=Displayed;	Qy	121 TSSYQPLPLENDCATAGTCBHVSGWGITNHPRNPPDILQCLNLSTIVSHATCHCGVYPGR1
CC	IsoId=060259-1; Sequence=vSP 005401;	Db	133 GSXKVPITSLADHETQEGKCTVSGWGTOTSPPRNFDLNCALVRKIPQRKCBDAVPGQ1	
CC	-!- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the pancreas while isoform 2 is expressed in adult brain and hippocampus. Both forms are also found in fetal brain and placenta. Not detected in kidney, spleen, liver and lung.	Qy	181 TSNMVACGGVPGODAAGDGSGLPVLICGVLQGLYVSNGVGPCQDGIPPOVTTICKYWD	
CC	-!- SIMILARITY: Belongs to Peptidase family S1. Kallikrein subfamily.	Db	193 TDGAVVACSSKGADTICQDSGGLVDCALOGITSGS-DPCGRSDKEGVTNICRYLDW	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Qy	241 IRMIM 245	
CC	DR MEROPS; S01:244; -;	Db	252 IKRII 256	
CC	DR Genew; HGNC:6369; -;			
CC	DR MIM; 605644; -;			
CC	DR GO; GO:0005236; P: serine-type peptidase activity; TAS.			
CC	DR GO; GO:0003739; P: neurogenesis; TAS.			
CC	DR InterPro; IPR00303; Cys_ser_trypsin.			
CC	DR InterPro; IPR001254; Peptidase_S1.			
CC	DR InterPro; IPR001314; Peptidase_S1A.			
CC	DR Pfam; PF00089; trypsin; 1.			
CC	DR PRINTS; PRO0722; CHYMOTRYPSIN.			
CC	DR SMART; SM00020; TRYD_SPC; 1.			
CC	DR PROSITE; PS50240; TRYSIN_DOM; 1.			
CC	DR PROSITE; PS00134; TRYSIN_HIS; 1.			
CC	DR PROSITE; PS00135; TRYSIN_SER; 1.			
KW	Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;			
KW	Alternative splicing.			
FT	SIGNAL 1 28			
FT	PROPEP 29 32		POTENTIAL.	
FT	CHAIN 33 260		BY SIMILARITY.	
FT	ACT SITE 73 73		NEUROPSIN.	
FT	ACT SITE 120 120		CHARGE RELAY SYSTEM (BY SIMILARITY).	
FT	ACT SITE 212 212		CHARGE RELAY SYSTEM (BY SIMILARITY).	
FT	DISTRPTD 39 173		CHARGE RELAY SYSTEM (BY SIMILARITY).	
FT	DISTRPTD 58 74		BY SIMILARITY.	
FT	DISTRPTD 145 246		BY SIMILARITY.	
FT	DISTRPTD 152 218		BY SIMILARITY.	
FT	DISTRPTD 184 198		BY SIMILARITY.	
FT	DISTRPTD 208 233		BY SIMILARITY.	
FT	CARBONYD 110 110		N-LINKED (GLCNAC-.) (POTENTIAL).	
FT	VARSPLIC 23 23		WRSNPLPAA (In isoform 2).	
FT	SEQUENCE 260 AA; 28048 MW; EP432E5B8C83B660 CRC64;		/FTId=VSP 005401.	
FT	Query Match Score 45.9%; Length 260;			
FT	Best Local Similarity 50.2%; Mismatches 93; Indels 5; Gaps 3;			
FT	Matches 123; Conservative 24; Mismatches 93; Indels 5; Gaps 3;			
Qy	5 IPLL--CVIGLSQATTPKIPFNGTECRNSPQWQCLPFGTSLRCGVVLIDHRWLTAA 61			
Db	13 MFLULGSGAWAGHSRAQBDKVGGHEQPHSQPWQAOALPQQLQCGVLYGGNNWLTAA 72			
Qy	62 HCGSRTRWVLGEHSLSOLDWTEQIRHSGFSYTHGYLGASt-SHEIDLRLRLRPLPVRY 120			
Db	73 HCKCPRTVRLGDHSLOQKDFQEIPVWQSIPHCYNTNSDVBDHNFMLLQLRQAS1 132		"Characterization of recombinant and brain neuropeptides, a	

RT plasticity-related serine protease.";
 RL J. Biol. Chem. 273:11189-11196(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 MEDLINE=9313451; PubMed=99335620;
 RX Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
 RA Shiosaka S., Hakoshima T.;
 RA "Crystal structure of neuropsin, a hippocampal protease involved in
 kindling epileptogenesis";
 RT J. Biol. Chem. 274:4220-4224(1999).
 CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 hippocampal plasticity. Has a strong proteolytic activity against
 fibronectin.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
 fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
 fluoride.
 CC -!- TISSUE/SPECIFICITY: Expressed specifically in the limbic system of
 mouse brain and is localized at highest concentration in pyramidal
 neurons of the hippocampal CA1-3 subfields.
 CC -!- MASSS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGB=29-260.
 CC -!- MASSS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGB=33-260.
 CC -!- SIMILARITY: Belongs to Peptidase family S1. Kallikrein subfamily.
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC DR EMBL: D30785; BAA06451_1; -.
 CC DR EMBL: AB032202; BAAB2435_1; -.
 CC DR PIR: BC05895; AAH5895_1; -.
 CC DR PIR: 156559; 156559.
 CC DR INPM: 23-MAR-99.
 CC DR MBROPS; S01_24; -.
 CC DR MGDB: MG1_892018; K1K8.
 CC DR InterPro: IPR009003; Cys_Ser_trypsin.
 CC DR InterPro: IPR011254; Peptidase_S1.
 CC DR InterPro: IPR001314; Peptidase_S1A.
 CC DR Pfam: PF00089; trypsin_1.
 CC DR PRINTS; PR00722; CHMOTRIPSIN.
 CC DR SMART; SM00020; TRYSP_SPC_1.
 CC DR PROSITE; PS500240; TRYPSIN_DOM; 1.
 CC DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine_protease; Glycoprotein; Zymogen; Signal;
 KW 3D-structure.
 FT SIGNAL 1 28
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT SITE 73 73
 FT ACT SITE 120 120
 FT ACT SITE 212 212
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT CARBOHYD 110 110
 FT STRAND 34 34
 FT STRAND 37 38
 FT TURN 41 42
 FT TURN 45 46
 FT STRAND 47 52
 FT STRAND 53 54
 FT STRAND 55 64
 FT TURN 65 66

FT STRAND 67 70
 FT HELIX 72 74
 FT STRAND 80 83
 FT STRAND 87 87
 FT TURN 88 89
 FT STRAND 96 98
 FT STRAND 100 105
 FT TURN 107 108
 FT TURN 114 115
 FT TURN 118 119
 FT STRAND 122 126
 FT STRAND 140 141
 FT TURN 148 149
 FT STRAND 151 156
 FT STRAND 170 170
 FT STRAND 172 178
 FT HELIX 181 187
 FT TURN 189 191
 FT TURN 194 195
 FT STRAND 196 200
 FT TURN 202 203
 FT STRAND 206 206
 FT TURN 209 210
 FT TURN 212 213
 FT STRAND 215 218
 FT TURN 219 220
 FT STRAND 221 228
 FT STRAND 235 235
 FT TURN 236 237
 FT STRAND 238 238
 FT STRAND 240 244
 FT HELIX 245 256
 SQ SEQUENCE 260 AA; 285/23 MW; B65F6P6BB37CD60E CRC64;
 CC

Query Match 45.3%; Score 622.5; DB 1; Length 260;
 Best Local Similarity 49.0%; Pred. No. 5_1e-44;
 Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

Qy 5 IPIIICV--IGLSQAAATPKIENCTEGCRNSQPHVGLPFGTSIURGGVLLDHRWVLTAA 61
 Db 13 ILLIFPMGAWAGLTAQGSKILBGRBCIPHSQPQKDALFOGERLICGGVLYGDRWVLTAA 72

Qy 62 HCGSGGRYWRLGEISLSQDWTEQRHSGSVTHYLGAS-TSHEDDLRLRLPLPVRY 120
 Db 73 HCKRKQKVSYRLGDHSLSQSRQKOPERIQVQAOSHNCYNNNPBDISHDMLRLQNSANL 132

Qy 121 TSSVQPLPLNDCATAGTECHVSGGITNHPRNPDPDILQLNLNSVSHATCHGTPGRI 180
 Db 133 GDKVTFPVQLANLCPTRVQKCLTISGGTVTSQENPNTLNCAEVKLYSONKCRAYPGK 192

Qy 181 TSNNYCAGGYPGODACQGDSGGPAPVCGVYQVQGLVWSGSVCPGQDGIPGVTTYICKXVDW 240
 Db 193 TGAACAGSSRGADTCQGDSEGPVLCGMLQGITSWGS-DECQKPBKPGVTKICRYTTW 251

RESULT 4
 NRPN RAT ID NRPN RAT STANDARD; PRT; 260 AA.
 AC 088780; DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 DB protease 1).
 GN K1KB OR PRSS19 OR NRPN OR BSP1.
 OS Rattus norvegicus (Rat).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

DB	254	KTM 256
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Fischer; TISSUE=Brain;	
RX	MEDLINE=98349725; PubMed=9725241;	
RA	"Serine proteases in rodent hippocampus." ; Davies B.J., Pichard B.S., Stein M., Morris R.G.M., Lache R. ; J. Biol. Chem. 273:23004-23011(1998).	
RL	-	
CC	- FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against fibronectin (By similarity). Catalytic activity: Preferential cleavage: Arg- . Lys- .	
CC	- SUBCELLULAR LOCATION: Secreted (By similarity).	
CC	- TISSUE SPECIFICITY: Restricted to hippocampus.	
CC	- SIMILARITY: Belongs to peptidase family SI. Kallikrein subfamily.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-	
DR	EMBL: AJ005641; CNA06643.1; - . HSMP; Q61955; INPM.	
DR	M3ROPS: S01_244; - .	
DR	InterPro: IPR000003; Cys_Ser_trypsin.	
DR	InterPro: IPR001254; Peptidase_SI.	
DR	InterPro: IPR001314; Peptidase_SIA.	
DR	Pfam: PF00089; CRYTPN, 1.	
DR	PRINTS: PRO0722; CRYMOTRYPIN.	
DR	InterPro: IPR00098; CRYTPN, 1.	
DR	SMART: SM00020; TRYPSIN.	
DR	PROSITE: PS50240; TRYPSIN; DOM; 1..	
DR	PROSITE: PS00134; TRYPSIN_HIS; 1..	
DR	PROSITE: PS00135; TRYPSIN_SER; 1..	
KW	Hydrolyase, Serine protease, Glycoprotein, Zymogen, Signal.	
FT	SIGNAL 1 28	
FT	PROPEP 29 32	
FT	CHAIN 31 260	
FT	ACT_SITE 73 73	
FT	ACT_SITE 120 120	
FT	ACT_SITE 212 212	
FT	DISULFID 39 173	
FT	DISULFID 58 74	
FT	DISULFID 145 246	
FT	DISULFID 152 218	
FT	DISULFID 184 198	
FT	DISULFID 208 233	
FT	CARBONYD 110 110	
SQ	SEQUENCEB 28510 MW; 58DP4F0602A0B75 CRC64; 260 AA;	
Qy	Query Match 45.24%; Score 621.5; DB 1; Length 260;	
Qy	Best Local Similarity 48.67%; Pred. No. 6.1e-44; Matches 118; Conservative 32; Mismatches 90; Indels 3; Gaps 3;	
Db	5 IFLLLL-CVGLHSQAAATPKIENGTECBGRNSOPQVGLPFGTSLSRGVYLIDHRWLVTAHC 63	
Db	15 LFLMLGAWAGLTRAQSKSLKEQBCKPHSQWPQTALPGERIVCGVYLGDRWLVTAHC 74	
Qy	64 SGSPRYHPLGHSHLSQDWTBIRHSGFSVTHPGYLGAS-TSHEDHLRLPLPVRTS 122	
Qy	75 RKKDKYSTRGLDESLQRKDEPQBIQVARSIOHPCFNSNPBHDIMLRLQNSANLGD 134	
Db	123 SVQPLPLPNDCATAGTECHVSGGITINHPRNPPDQLQCLNUISVHATCHGVYPRITs 182	
Db	135 KVKPFBLANLCKPGQKLIISSGTTSQPNPNTLCAPIYKIQSONKCRAYPKITE 194	
Qy	183 NMVCAAGGVPGPQDAGCDSGGPLVCGGYLOGIWSGSVGPCCGODGIPSYUTYICKYWDWIR 242	
Db	195 GRVACGSSNGADTCQGDSPKPLVNGVQGITWGS-DPCGKPKEPKVYTKCIRTNWIK 253	
Qy	243 MM 245	

CC	IsoId=09H2R5-3; Sequence=vsp_005406; vsp_005407;	Db	181 DKSYPGRLLNTMVCAGAAGRASSC6DGGPLVCGGILQGLIVSGDV-PCDNTRKPGVY 239
CC	-!- TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also expressed in the prostate, salivary, and adrenal glands and in the colon, testis and kidney.	Qy	232 TYCKYVNDWIRMRN 248
CC	-!- SIMILARITY: Belongs to peptidase Family S1. Kallikrein subfamily.	Db	240 TRVCHYLEWIRETMKRN 256
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL: AF242195; ARG09469_1; -	RESULT 7	TRY3_CHICK STANDARD; PRT; 248 AA.
CC	EMBL: AF242195; ARG09410_1; -	ID TRY3_CHICK	Q96129; Rel. 35, Created)
CC	DR GO: GO-0004525; P:serine-type endopeptidase activity; NAS.	AC	DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC	DR GO: GO-0006508; P:proteolysis and peptidolysis; NAS.	AC	DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC	DR InterPro: IPR009003; Cys_Ser-trypsin.	DB	DB Trypsin IR-PAGE precursor (BC 3.4.21.4).
CC	DR InterPro: IPR001254; Peptidase_S1.	OS	OS Gallus gallus (Chicken).
CC	DR InterPro: IPR001314; Peptidase_S1A.	OC	OC Buteo buteo; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC	PRINTS: PR00722; CHYMOTRYPSIN.	OC	OC Gallus.
CC	DR PROSITE: PS00240; TRYPSIN_DOM; 1.	NCBI_TAXID:9031; [1]	OX NCBI_TAXID=9031;
CC	DR PROSITE: PS00134; TRYPSIN_HIS; 1.	RN	RP SEQUENCE FROM N.A.
CC	DR PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.	RC	RC TISSUB=Pancreas;
CC	KW Hydrolase; Serine_protease; Glycoprotein; Signal; Zymogen;	RX	RX MEDLINEB=95251611; PubMed=7733885;
CC	KW Alternative splicing.	RA	RA Wang K.; Gan L.; Lee I.; Hood L. B.;
PT	SIGNAL 1 16	RT RT "Relation and characterization of the chicken trypsinogen gene family.";	RT RL Biochem. J. 307:471-479(1995).
PT	PROPEP 17 21	CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Xaa, Lys- -Xaa.	CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
PT	CHAIN 22 256	CC -!- SUBCELLULAR LOCATION: Extracellular.	CC -!- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.
PT	ACT SITE 62 62	CC -!- SIMILARITY: Belongs to peptidase family S1.	CC -!- SIMILARITY: Belongs to peptidase family S1.
PT	ACT SITE 106 106	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
PT	ACT SITE 209 209	CC DR PROSITE: PR001335; TRYPSIN_SER; Multigene family.	CC DR PROSITE: PR001335; TRYPSIN_SER; Multigene family.
PT	CARBONYD 171 171	CC DR HSSP: SS5066; SS5066.	CC DR HSSP: SS5066; SS5066.
PT	CARBONYD 232 232	CC DR MEROPS: S01.151; IDPO.	CC DR MEROPS: S01.151; IDPO.
PT	VARSPLIC 122 206	CC DR InterPro: IPR009003; Cys_Ser_trypsin.	CC DR InterPro: IPR001254; Peptidase_S1.
PT	VARSPLIC 122 256	CC DR SMART: SM00020; TRYSPC; 1.	CC DR SMART: SM00020; TRYSPC; 1.
PT	VARSPLIC 161 161	CC DR PROSITE: PS001340; TRYPSIN_DOM; 1.	CC DR PROSITE: PS001340; TRYPSIN_DOM; 1.
PT	VARSPLIC 162 256	CC DR PROSITE: PS001335; TRYPSIN_HIS; 1.	CC DR PROSITE: PS001335; TRYPSIN_HIS; 1.
PT	CONFLICT 147 160	CC DR Pfam: PF00089; Trypsin, 1.	CC DR Pfam: PF00089; Trypsin, 1.
PT	SEQUENCE 256 AA; 28087 MW;	CC DR PRINTS: PR00722; CHYMOTRYPSIN.	CC DR PRINTS: PR00722; CHYMOTRYPSIN.
PT	Missing (In isoform 3).	CC DR SMART: SM00020; TRYSPC; 1.	CC DR SMART: SM00020; TRYSPC; 1.
PT	/PTId=VSP 005404.	CC DR PROSITE: PS001335; TRYPSIN_SER; 1.	CC DR PROSITE: PS001335; TRYPSIN_SER; 1.
PT	Missing (In isoform 2).	CC DR Hydrolease; Serine_protease; Digestion; Pancreas; Zymogen; KW Calcium-binding; signal; Multigene family.	CC DR Hydrolease; Serine_protease; Digestion; Pancreas; Zymogen; KW Calcium-binding; signal; Multigene family.
PT	/PTId=VSP 005405.	FT SIGNAL 1 16	FT SIGNAL 1 16
PT	V->G (In isoform 3).	FT PROPEP 17 25	FT PROPEP 17 25
PT	/PTId=VSP 005406.	FT CHAIN 26 248	FT CHAIN 26 248
PT	Missing (In isoform 3).	FT ACT_SITE 65 65	FT ACT_SITE 65 65
PT	/PTId=VSP 005407.	FT METAL 77 77	FT METAL 77 77
PT	SHNBPGTAGSPRSQ-> PLSSP (IN REF. 2).	FT METAL 79 79	FT METAL 79 79
PT	BSEBF860227685 CRC64;	FT METAL 82 82	FT METAL 82 82
PT	Best Local Similarity 47.1%; Pred. No. 4.2e-42; Length 256;	FT METAL 87 87	FT METAL 87 87
PT	Matches 121; Conservative 32; Mismatches 81; Indels 16; Gaps 6;	FT ACT_SITE 109 109	FT ACT_SITE 109 109
Qy	5 IFLILCVLGSLQAT- PKIPIKGTECGNSOPHQVGLPFGTSLSRGGVYLDRHWRVTAH 62	FT ACT_SITES 202 202	FT ACT_SITES 202 202
Db	3 LLLTSLSPULASTAAQGDQDILEGDECAPSQPKQVALYERGRTRNGASLISPHWLSAH 62	FT DISULFID 32 162	FT DISULFID 32 162
Qy	63 CGSGRYWVRLGHSLSQWLTBEQRHSGSVTHGGLGASTSHEDLRLRLRPLPVRTS 122	FT DISULFID 50 66	FT DISULFID 50 66
Db	63 CQSRFMTRFLGEANLRKGDPQLRTRTSVSPHRY-EARSHRDIMLRLVQPARLNP 120		
Qy	123 SYOPLPLPINDCATAGTCVHSGRGTNH-----PRN-PPPDILQCLNLNSIVSHATC 172		
Db	121 QVRAVLPRCPHQBACVSGRLVSHBTPGTAGSPRSQVSLEPTLCAANISIISDTSIC 180		
Qy	173 HGVPGRITSNMVCRGGV- PGQDRCIQGDSGGPLVCGGVLQGLVSGWSVPCGDGIPGVY 231		

FT	DISUFID	134	235	BY SIMILARITY.
FT	DISUFID	141	208	BY SIMILARITY.
FT	DISUFID	173	187	BY SIMILARITY.
FT	DISUFID	198	222	BY SIMILARITY.
SITE		196	196	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SEQUENCE	248 AA;	26622 MW;	E5E6B01622B9B CTC64;	
Query Match		41.4%	Score 569.5; DB 1; Length 248;	
Best Local Similarity	47.5%	Pred No. 1e-39; Mismatches 39; Indels 11; Gaps 6;		
Matches	116;	Conservative	39;	
Qy	5 IPI10091GLS-----QAAFPKIPNTECBGRNSQPKQVGLFEFTSARCGGVFLIDIRWWTJ 59			
	: : : : : : : : : : : : : : : :			
Db	4 LFLFLSCLGAAVAPFGCADDKIVGTYCTCPHEVSPIQVSLSNGYHFCGGSILNSQWVL 62			
Qy	60 AAHCSSCSRNVRLGEISLSQLDWTEIRHSFSPVTHPGYLGASTSHEDFLRLRLLPVR 119			
	: : : : : : : : : : : : : : :			
Db	63 ARHCVKSRIQTRIGENMIDQEDSEPTVTRASSSVTIRPKY-SSITIANDMLIKLASVE 120			
Qy	120 VTSSYVPLPLPNDCATAGTECHVSGMGITINHPRNPDPDQIOLATISIVSHATCHGVPGR 179			
	: : : : : : : : : : : : : : :			
Db	121 YSADICPQLPSSCARAGTBELSGNTGNTLNGTQNLQCLANAPLSDQBCQAYPGD 180			
Qy	180 ITSMWMCAGGP-GDQACQGDGGPVGCGWLGQIWSKGSGVPCGCGDGPGVYTTICRKYV 238			
	: : : : : : : : : : : : : : :			
Db	181 ITSMWMCAGGP-GDQACQGDGGPVGCGWLGQIWSKGSGVPCGCGDGPGVYTTICRKYV 238			
Qy	239 DWIR 242			
	: :			
Db	239 DWIQ 242			
RESULT 8				
	KLK1 HUMAN	STANDARD;	PRT;	251 AA.
ID	KLKB HUMAN			
AC	Q9PQ53;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-DEC-2003 (Rel. 41, Last annotation update)			
DB	Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6)			
DB	(KLK16).			
GN	KLK14 OR KLK16			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
[1]	SEQUENCE FROM N.A.			
RA	Youself G.M., Diambandis B.P.;	SEQUENCE FROM N.A.		
RA	"Molecular characterization, mapping, and tissue expression of KLK16,"			
RA	a hormonally regulated kallikrein-like gene."			
RA	Submitted (JUN-1999) to the RMBL/GenBank/DDJB databases.			
[2]	SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.			
RA	Cooper J.D., Bui L.T., Rae P.K., Harvey T.J., Myers S.A.,	SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.		
RA	Burkhardt-Schultz K., Gordon L., Diaz J., Ramirez M., Stilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garres J.,			
RA	Dangano L., Briler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,			
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,			
RA	Olsen A.S., Carrasco A.V.			
[3]	SEQUENCE FROM N.A.			
RA	Lamerdin J.E., McCready P.M., Skowronski B., Viswanathan V.,	SEQUENCE FROM N.A.		
RA	Burkhardt-Schultz K., Gordon L., Diaz J., Ramirez M., Stilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garres J.,			
RA	Dangano L., Briler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,			
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,			
RA	Olsen A.S., Carrasco A.V.			
RA	"Sequence analysis of chromosome 19q13.4,"			
RA	Submitted (OCT-2000) to the RMBL/GenBank/DDJB databases.			

Db	179	YPTITPGVCA-GPQGGKDSQQGFLVCRGOLGLYSWG-MERCALPGYPSVYT	N	236
Qy	234	ICKYDWMIRMMRN 247		
Db	237	LCKTRSWEEETMRD 250		
RESULT 9				
KLK9_HUMAN				
ID	KLK9_HUMAN	STANDARD;	PRT:	250 AA.
AC	Q9URQ9;			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	20-FEB-2003	(Rel. 41, Last annotation update)		
DB	Kallikrein_9 precursor (BC 3.4.21.-)	(Kallikrein-like protein 3)	(KLK-L3).	
DB	GN	GN		
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
[1]				
RN				
RP	SEQUENCE FROM N.A.			
RX	Medline:20118156; PubMed:10652563;			
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.,			
RA	"The expanded human kallikrein gene family: locus characterization and			
RT	"Identification of novel human kallikrein-like genes on chromosome			
RT	19q13.3-q13.4.";			
RT	molecular cloning of a new member, KLK-L3."			
RT	Anticancer Res. 19:2843-2852 (1999).			
RL				
RN				
RP	SEQUENCE FROM N.A.			
RX	Medline:20247258; PubMed:10783266;			
RA	Yousef G.M., Diamandis E.P.,			
RA	"The expanded human kallikrein gene family: locus characterization and			
RT	"Identification of novel human kallikrein-like genes on chromosome			
RT	19q13.3-q13.4.";			
RT	molecular cloning of a new member, KLK-L3."			
RT	Anticancer Res. 19:2843-2852 (1999).			
RL				
RN				
RP	SEQUENCE FROM N.A.			
RX	Medline:20510030; PubMed:11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McChraig J.,			
RA	Moss P., Paerl B., Wang K.,			
RA	"Sequencing and expression analysis of the serine protease gene			
RT	"Sequence analysis of chromosome 19q13 region.";			
RT	cluster located in chromosome 19q13 region.";			
RL				
RN				
RP	SEQUENCE FROM N.A.			
RA	Lamerdin J.B., McCready P.M., Skowronski E., Viswanathan V.,			
RA	Burkhardt-Schulz K., Gordon L., Diaz J., Ramirez M., Strilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.,			
RA	Danganan L., Euler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Andreise T., Trantheim M., Attix C., Amico-Teller G., Coeffield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Qian G., Kronmiller B.,			
RA	Arellano A., Sanders C., O'D., Nolan M., Trong S., Kobayashi A.,			
RA	Olsen A.S., Carrano A.V.,			
RT	"Sequence analysis of chromosome 19q13.4.";			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.			
CC	- - SUBCELLULAR LOCATION: Secreted (Probable).			
CC	- - TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal			
CC	cord.			
CC	- - SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch .			
CC				
DR	EMBL: AP135026; ADD26427; 2;			
DR	DR			
DR	EMBL: AF243525; AAC33362; 1;			
DR	DR			
DR	EMBL: AC011473; AAC23255; 1;			
DR	DR			
DR	HSSP: P00763; 1DP0;			

RX	MEDLINE=20229789; PubMed=10766816;	Qy	13 GLSQAATPKIFN-----GTEGGRNSOPWQVGLPEFTSLRCCGVLLIDHRWVLTAAH 62
RA	Yousef G.M.; Chang A.; Diamandis E.P.;	Db	18 GVSQESS-KVINTNTGTSQGFLPFGYTCPHSOPWQAILVQGRLLCGVLLVTPKWLTAHH 76
RT	"Identification and characterization of KLK-L4, a new kallikrein-like gene that appears to be down-regulated in breast cancer tissues.";	Qy	19 CSGSRSTWVRLGEHSLQLDWTEQRHSQFSTHGYLCAST-SHEFDLRLRLRLPVRV 120
RL	J. Biol. Chem. 275:11891-11898(2000).	Db	63 CSGSRSTWVRLGEHSLQLDWTEQRHSQFSTHGYLCAST-SHEFDLRLRLRLPVRV 136
RN	[2]	77 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136	
RP	SEQUENCE FROM N.A.	Qy	78 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RA	Lamerdin J.E.; McCready P.M.; Skowronski B.; Viswanathan V., Burkhardt-Schultz K.; Gordon L.; Dias J.; Ramirez M.; Silwagen S.,	Db	79 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RA	Phan R.; Velasco N.; Dangaran L.; Regala W.; Terry A.; Brower A.; Garnes J.J., Dangaran L.; Erler A.; Christensen M.; Georgeiou A.; Avila J.; Liu S., Andreise T.; Frankheim M.; Attix C.; Amico-Keller G.; Coefield J., Duarte S.; Lucas S.; Bruce R.; Thomas P.; Quan G.; Krommiller B., Arellano A.; Sanders C.; Ow D.; Nolan M.; Trong S.; Kobayashi A., Olsen A.S.; Carrano A.V.;	Qy	80 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RA	"Sequence analysis of chromosome 19q13.4."	Db	81 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RL	Submitted (OCT-2000) to the EMBL/GenBank/DDJB databases.	Qy	82 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RN	[3]	Db	83 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RP	SEQUENCE OF 1-180 FROM N.A.	Qy	84 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RC	TISSUE=UTERUS; Ansorte W.; Wirkner U.; Newes H.-W.; Gassendorfer J.; Wiemann S.;	Db	85 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDJB databases.	Qy	86 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
RL	-!- SUBCELLULAR LOCATION: Secreted (Probable).	Db	87 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
CC	-!- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and salivary gland.	Qy	88 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
CC	-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.	Db	89 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
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CC	or send an email to license@isb-sib.ch).	Db	91 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	EMBL; AF135024; AAD26425.2; -.	Qy	92 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	EMBL; AC01473; AAG22259.1; -.	Db	93 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	EMBL; AL050220; CAB13320; -.	Qy	94 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	HSSP; P0763; 1DPO.	Db	95 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	MIBIDS; S01.306; -.	Qy	96 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	MINI; 60505; -.	Db	97 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	GO; GO:000576; :extracellular; NAS.	Qy	98 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	GO; GO:0004252; F:serine-type endopeptidase activity; NAS.	Db	99 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	GO; GO:000508; P:proteolysis and peptidolysis; NAS.	Qy	100 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	InterPro; IPR00903; Cys_Ser_trypsin.	Db	101 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	InterPro; IPR001254; Peptidase_S1.	Qy	102 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	InterPro; IPR001314; Peptidase_S1A.	Db	103 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	Pfam; PF00989; trypsin_1.	Qy	104 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	PRINTS; PRO0722; CHYMOTRYPSIN.	Db	105 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	SMART; SM00020; TRIP_SPC_1.	Qy	106 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	Db	107 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	Qy	108 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	Db	109 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
KW	Hydrolyase; Serine protease; Signal.	Qy	110 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SIGNAL 1 16	Db	111 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CHAIN 17 277	Qy	112 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 76 76	Db	113 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Qy	114 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Db	115 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Qy	116 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Db	117 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Qy	118 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Db	119 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Qy	120 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Db	121 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Qy	122 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Db	123 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA; 30570 MW;	Qy	124 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Db	125 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Qy	126 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Db	127 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Qy	128 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Db	129 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Qy	130 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Db	131 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Qy	132 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Db	133 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Qy	134 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Db	135 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Qy	136 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Db	137 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Qy	138 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Db	139 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Qy	140 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Db	141 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Qy	142 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Db	143 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Qy	144 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Db	145 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Qy	146 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Db	147 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Qy	148 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Db	149 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Qy	150 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Db	151 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Qy	152 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Db	153 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Qy	154 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Db	155 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Qy	156 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Db	157 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Qy	158 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Db	159 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Qy	160 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Db	161 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Qy	162 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Db	163 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Qy	164 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Db	165 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Qy	166 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Db	167 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Qy	168 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Db	169 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Qy	170 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Db	171 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Qy	172 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Db	173 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Qy	174 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Db	175 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Qy	176 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Db	177 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Qy	178 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Db	179 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Qy	180 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Db	181 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Qy	182 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Db	183 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Qy	184 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Db	185 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Qy	186 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Db	187 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Qy	188 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Db	189 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Qy	190 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Db	191 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Qy	192 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Db	193 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Qy	194 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Db	195 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Qy	196 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Db	197 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Qy	198 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Db	199 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Qy	200 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Db	201 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Qy	202 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Db	203 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Qy	204 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Db	205 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Qy	206 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Db	207 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 214 239	Qy	208 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 30 30	Db	209 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CARBONYD 225 225	Qy	210 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	CONFLICT 170 180	Db	211 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	SEQUENCE 277 AA;	Db	212 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 124 124	Qy	213 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	ACT SITE 218 218	Db	214 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 42 178	Qy	215 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 61 77	Db	216 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 157 224	Qy	217 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELOSPVQL 136
FT	DISULFID 189 203	Db	218 CLKEGLKVLGKHALGRVEAGEQEVVHSIIPHBYTRSPHTLNHDIMLELO

SIGNAL	1	15	BY SIMILARITY.
PROPEP	16	25	ACTIVATION PEPTIDE (BY SIMILARITY).
CHAIN	26	248	TRYPSIN 1-P38.
ACT_SITE	65	65	CHARGE RELAY SYSTEM (BY SIMILARITY).
METAL	77	77	CALCIUM (BY SIMILARITY).
METAL	79	79	CALCIUM (VIA CARBONYL OXYGEN) (BY SIMILARITY).
DISULFID	87	87	CALCIUM (BY SIMILARITY).
ACT_SITE	109	109	CHARGE RELAY SYSTEM (BY SIMILARITY).
ACT_SITE	202	202	CHARGE RELAY SYSTEM (BY SIMILARITY).
DISULFID	32	162	BY SIMILARITY.
DISULFID	50	66	BY SIMILARITY.
DISULFID	134	235	BY SIMILARITY.
DISULFID	141	208	BY SIMILARITY.
DISULFID	173	187	BY SIMILARITY.
DISULFID	198	222	BY SIMILARITY.
SITE	196	196	REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SEQUENCE	248 AA;	26087 MW;	78B79D06F15FOCB CRC64;
Query Match	41-23;	Score 566;	DB 1;
Best Local Similarity	45.8%;	Pred. No. 2e-39;	Length 248;
Matches 116; Conservative 39; Mismatches 86; Indels 12; Gaps 7;			
Dy	3 LSFLLCTLG----LQAAATPKIIFNGTECGANSQPYQVGLPEGTSLRGCGYLIDIRHN	56	
Dy	1 MKFLVLVAVLGVAYAAPPISDEDDKIVGGYSCARSAAAPQVSNSNGYHP-CGGSLSISSCW	59	
Dy	57 VLTAAHCSGRSYWVRLGEHSLSSLQDTEIRHSGFSVTPLGCASTSHEDLRLRRL	116	
Dy	60 VLSAAHCTYSVQLRGEINLAADGSEFISSKRVIRSGY-NANTIN-NDIMLIRSK	117	
Dy	117 PVRVTSVQVPLPLENDCATAGTECHVSGGITNHPRNPPDQLQCLNLISIVSHATCHGW	176	
Dy	118 AATLNNSYNTVPLPSCSVTGAFTCLLISIGNTLSSGLSLPDVQLCLNAPEVSSQCSSAY	177	
Dy	117 PGRITSANMCAAGGY-PGQACOQEDGGPPLVCGGVLQGLISWGSVGPCCGGIPEVYTIC	235	
Dy	118 PGRITSNMICIGYLNGKSDCQEDGGPVTVCNGOLQGPVSWG-IG-CACKGYPEVYTIC	235	
Dy	236 KYWDWIRMIARNN 248		
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CC	use by non-profit institutions as long as its content is in no way	CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announces	CC	or send an email to license@isb-sib.ch).
CC	EMBL; U15155; AAA79812.1; -	DR	DR
CC	HSSP; P00763; 1DPO.	DR	DR
CC	MEROPS; S01_151; -	DR	DR
CC	InterPro; IPR009003; Cys_Ser_trypsin.	DR	DR
CC	InterPro; IPR001254; Peptidase_S1.	DR	DR
CC	InterPro; IPR001314; Peptidase_S1A.	DR	DR
CC	Pfam; PF0009; trypsin; 1.	DR	DR
CC	PRINTS; PR0072; CHYMOTRYPSIN.	DR	DR
CC	SMART; SM00020; TRYD_SPEC1.	DR	DR
CC	PROSITE; PS5040; TRYPsin_DOM; 1.	DR	DR
CC	PROSITE; PS00134; TRYPsin_HIS; 1.	DR	DR
CC	PROSITE; PS00135; TRYPsin_SER; 1.	DR	DR
CC	KW Calcium-binding_Signal; Multigene family.	KW	
CC	Calmodulin-binding_Signal; Multigene family.	KW	
CC	BY SIMILARITY.		
CC	FT SIGNAL 15	FT	
CC	FT PROPEP 16	FT	
CC	FT CHAIN 26	FT	
CC	FT ACT_SITE 65	FT	
CC	FT METAL 77	FT	
CC	FT METAL 79	FT	
CC	FT METAL 87	FT	
CC	FT ACT_SITE 109	FT	
CC	FT ACT_SITE 202	FT	
CC	FT DISULPID 32	FT	
CC	FT DISULPID 50	FT	
CC	FT DISULPID 134	FT	
CC	FT DISULPID 142	FT	
CC	FT DISULPID 173	FT	
CC	FT DISULPID 198	FT	
CC	FT SITE 196	FT	
CC	SEQUENCE 248 AA;	SEQUENCE	248 AA; CACF589912B23D98 CRC64;

RESULT 12		Best Local Similarity 45.5%; Pred. No. 2.4e-39; Matches 115; Conservative 41; Mismatches 85; Indels 19; Gaps 7	
TRY1	CHICK	STANDARD;	PRT; 248 AA.
090627;	TRY1_CHICK		
01-NOV-1997 (Rel. 35, Created)			
01-NOV-1997 (Rel. 35, Last sequence update)			
10-OCT-2003 (Rel. 42, Last annotation update)			
Trypsin I-Pi precursor (EC 3.4.21.4).			
Gallus gallus (Chicken).			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
NCBI_TaxID=9031;			
[1]			
SEQUENCE FROM N.A.			
TISSUE_Pancreas;			
MEDLINE=95251611; PubMed=7733885;			
Wang K., Gan L., Lee I., Hood L.E.; "Isolation and characterization of the chicken trypsinogen gene family." Biochem. J. 307:471-479 (1995).			
-I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Xaa-Lys-Xaa.			
-I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).			
-I- SUBCELLULAR LOCATION: Extracellular.			
-I- TISSUE SPECIFICITY: High levels are seen in the pancreas while lower levels are found in the liver, spleen and thymus.			
-I- SIMILARITY: Belongs to peptidase family S1.			
CC	CC	RESULT 13	
CC	CC	KLKS HUMAN	
CC	CC	ID Q9T337; Q9HBGB;	
CC	CC	STANDARD; PRT; 293 AA.	
CC	CC	AC DT 16-OCT-2001 (REL 40, Created)	
CC	CC	DT DT 16-OCT-2001 (REL 40, Last sequence update)	
CC	CC	DT DT 15-MAR-2004 (REL 43, Last annotation update)	
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	

DE Kallikrein 5 precursor [EC 3.4.21.-] (Stratum corneum trypic enzyme)
 DE (Kallikrein-like protein 2) [KLK-L2].
 GN KLK5 OR SKTP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI TaxID=9606;
 RN [1]
 RP SSEQUENC FROM N.A.
 RX TISSUE=Stratum corneum;
 MEDLINEB=90445563; PubMed=10514489;
 RA Brattand M., Egeland T.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4.";
 RL Anticancer Res. 19:2843-2852(1999).
 RN [2]
 RP SSEQUENC FROM N.A.; PubMed=10652563;
 RA Yousef G.M., Liao L.-Y., Diamandis E.P.;
 RT "Identification of novel human kallikrein-like genes on chromosome
 RT 19q13.3-q13.4.";
 RL Anticancer Res. 19:2843-2852(1999).
 RN [3]
 RP SSEQUENC FROM N.A.; PubMed=20510030;
 MEDLINEB=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J. J.,
 RA Moss B., Paer P., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]
 RP SSEQUENC FROM N.A.
 RX TISSUE=Ovary;
 MEDLINEB=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schulz B., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer M.A., Rubin G.M., Hong B.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquai Lano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay E.J., Hulyk S.W.,
 RA Villanueva D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnetzer A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC "- FUNCTION: May be involved in desquamation.
 CC "- SUBCELLULAR LOCATION: Secreted.
 CC "- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
 CC "- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

DR MEROPS; SD1_017; -;
 DR Genbank; HGNC:6366; KLKS.
 DR MIM: 605633; -;
 DR GO: 0005615; C:extracellular space; TAS.
 DR GO: 0004252; P:serine type endopeptidase activity; NAS.
 DR GO: 0008544; P:epidermal differential proteolysis; TAS.
 DR GO: 0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Cys Ser trypain.
 DR InterPro; IPR01254; Peptidase_S1.
 DR InterPro; IPR01314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHMTRYPSIN.
 DR SMART; SM00020; TRYSPIN_1.
 DR PROSITE; PS50340; TRYSPIN_DOM; 1.
 DR PROSITE; PS00344; TRYSPIN_HIS; 1.
 DR PROSITE; PS00135; TRYSPIN_SER; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Signal.
 PT SIGNAL 1 22
 PT CHAIN 1 23
 PT ACT SITE 108 293
 PT ACT SITE 153 108
 PT DISULFID 245 153
 PT DISULFID 73 245
 PT DISULFID 93 206
 PT DISULFID 178 206
 PT DISULFID 185 209
 PT DISULFID 251 245
 PT DISULFID 231 245
 PT DISULFID 241 266
 PT CARBOHYD 69 69
 PT CARBOHYD 173 173
 PT CARBOHYD 208 208
 PT CARBOHYD 252 252
 PT CONFLICT 25 56
 SQ SEQUENCE 293 AA; MISSING [IN REF. 3];
 SQ SEQUENCE 320 AA; D94C92F509E83946 CRC64;
 Query Match 41.1%; Score 564.5; DB 1; Length 293;
 Best Local Similarity 45.3%; Pred. No. 3.2e-39;
 Matches 107; Conservative 41; Mismatches 83; Indels 5; Gaps 4;
 Qy 15 SQAPKPKIPTGTCGRNSQPKQVG-LFGTSRCCGVLLDVRWVLTAAHCGSRVPRVLG 73
 RA :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 RA 60 SDDSSSRITNGSDCDMHTQPOAALLRPQLCYGAVINHQMLTAAHCRKVKPVRLG 119
 Qy 74 EHSLSQLDNTAEQIRHSQGP-SVTHPGLGASTSHEDIDLRLRLRPLRVTSVQPPLPND 132
 RA :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 RA 120 HYLSLSEVYBSQQMQVQGVSPIPHGPI-SHPGHSDMLIGNRTRPDKVRPVNHH 177
 RA 133 CATACTGCAGTGAGTNTNHPNPDPOLQCLNTSVIYSHATCHGIVYPERITSNMYCAGVPG 192
 RA :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 RA 178 CPSAGTKCLGWTGKTSPQHVKPVQLNATISQSQRKCEDAYPKQDIDMPCAQDKAG 237
 Qy 193 QDACCQDGSQPLWICGCVLQGLVSSVSGPCQGDQPGTYTICKYDWMIMRN 248
 RA :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 DB 238 RDSCQDSSGGevvvcnscsQGLvsswdy-PCARPNEPGVTLCKFTKWIQTQAN 292
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epithelium;

RESULT 14
 KLKS_HUMAN STANDARD; PRT; 276 AA.
 ID KLKA_HUMAN STANDARD;
 AC O43240; Q99920; Q9GK9W9.
 DT 043240; Q99920; Q9GK9W9.
 CC 15-DEC-1998 (Rel. 37, Created)
 CC 15-DEC-1998 (Rel. 37, Last sequence update)
 CC 15-MAR-2004 (Rel. 43, Last annotation update)
 CC Kallikrein 10 precursor (EC 3.4.21.1) (Protease serine-like 1) (Normal
 CC epithelial cell-specific 1).
 CC Homo sapiens (Human).
 CC Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Epithelium;

RX MEDLINE:96320486; PubMed=8764136;
 RA Liu X.-L., Waeer D.E., Watanabe K., Band V.;
 RT "Identification of a novel serine protease-like gene, the expression of which is down-regulated during breast cancer progression.";
 RL Cancer Res. 56:3371-3379(1996).
 [2]

RN SEQUENCE FROM N.A.
 RX MEDLINE:98321170; PubMed=9647736;
 RA Luo L.-M., Herbrick J.A., Scherer S.W., Beatty B., Squire J.J.,
 RA Diamandis E.P.;
 RT "Structural characterization and mapping of the normal epithelial cell-specific 1 gene.";
 RT Biochem. Biophys. Res. Commun. 247:580-586(1998).
 RN [3]

RN SEQUENCE FROM N.A.
 RX MEDLINE:2010030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.J.,
 RA Moss P., Paepke B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [4]

RN SEQUENCE FROM N.A.
 RX MEDLINE:J.B.; McCready P.M., Skowronski B., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J.J.,
 RA Dargaman L., Brier A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coeffiel J.J.,
 RA Duarte S., Lucas S., Bruce P., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Sanders C., Ow D., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrasco A.V.;
 RT "Sequence analysis of chromosome 19q13.4";
 RL Submitted (Oct-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]

RN SEQUENCE FROM N.A.
 TISSUE=Uterus;
 RX MEDLINE:22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Shenaan C.P., Bhattacharyya S.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsusuna K., Farmer A.P., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Usdin T.B., Toshiiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J.,
 RA Botak S.A., McEwan P.J., McFernan K.J., Malek J.A., Gunnarsson P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Munny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heitton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimes J., Schmitz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywiński M.I., Skalska U., Smailus D.E.,
 RA Schnarch A., Schein J.B., Jones S.J.M., Marr M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]

RN CHARACTERIZATION,
 RX MEDLINE:99025548; PubMed=98099976;
 RA Goyal J., Smith K.M., Cowan J.M., Wazir D.E., Lee S.W., Band V.;
 RT "The role for NEST1 serine protease as a novel tumor suppressor.";
 RL Cancer Res. 58:4782-4786(1998).
 CC -1- FUNCTION: Has a tumor-suppressor role for NEST1 in breast and prostate cancer.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: Expressed in breast, ovary and prostate.
 CC -1- DEVELOPMENTAL STAGE: Down-regulated during breast cancer progression.
 CC -1- SIMILARITY: Belongs to Peptidase family SI. Kallikrein subfamily.

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 CC
 CC DR EMBL; ABB81602; 1; -
 CC DR EMBL; AR05481; ARC14266; 1; -
 CC DR EMBL; AR243527; ARG33363; 1; -
 CC DR EMBL; AC011473; ARG23256; 1; -
 CC DR EMBL; BCO02710; AHO02710; 1; -
 CC DR HSSP; P00763; 1DPO.
 CC DR MEROPS; S01.246; -
 CC DR Genew; HGNC:6358; KLK10.
 CC DR MINP; 602673; -
 CC DR GO; GO:0005576; C_extracellular; TAS.
 CC DR GO; GO:0008226; P_serine-type_peptidase_activity; TAS.
 CC DR InterPro; IPR009003; Cys_Ser_trypsin.
 CC DR InterPro; IPR001254; Peptidase_SI.
 CC DR InterPro; IPR01314; Peptidase_SI.
 CC DR Pfam; PF00083; trypsin_1.
 CC DR PRINTS; PR00722; CHYMOTRYPSIN.
 CC DR SMART; SM0020; TRYSP_1.
 CC DR PROSITE; PS50240; TRYSPIN_DOM; 1.
 CC DR PROSITE; PS00134; TRYSPIN_HIS; 1.
 CC DR PROSITE; PS00135; TRYSPIN_NEG.
 CC KW Hydrolase; serine_protease; Glycoprotein; signal; Anti-oncogene.
 CC FT SIGNAL; 1 30
 CC FT CHAIN; 31 276
 CC FT ACT_SITE; 86 86
 CC FT ACT_SITE; 137 137
 CC FT ACT_SITE; 229 229
 CC FT DISULFID; 52 162
 CC FT DISULFID; 71 87
 CC FT DISULFID; 263 BY SIMILARITY.
 CC FT DISULFID; 169 235 BY SIMILARITY.
 CC FT DISULFID; 201 215 BY SIMILARITY.
 CC FT DISULFID; 225 250 BY SIMILARITY.
 CC FT CARBOHYD; 39 39 N-LINKED '(GLCNAC. . .) (POTENTIAL).'
 CC FT CONFLICT; 50 50 A->L (IN REF. 3 AND 4).
 CC FT CONFLICT; 149 149 P->L (IN REF. 3 AND 4).
 CC SQ SEQUENCE; 276 AA; 30138 MW; 82A2507379BAB313 CRC64;
 CC SQ SEQUENCE; 276 AA; 30138 MW; 82A2507379BAB313 CRC64;
 CC Query Match 41.0%; Score 564;
 CC Best Local Similarity 45.9%; Pred. No. 3.3e-39;
 CC Matches 118; Conservative 29; Mismatches 92; Indels 18; Gaps 5;
 CC Qy 7 LLLCLGLGSQAA-----TPKIFNGTBCGRNSQPKQVGLPFCTSLRAGGHLIDHRRWV 57
 CC DB 23 LLMALQWAAEALPQNDRTRDPEAY-GAPCARGSPQVSLERLSPHCAGVLVDQSMV 81
 CC Qy 58 LTAIAHCSRSRYWRGHLSLSQDWTBIRHSGFSVTHGYLGAS-----TSBHDRL 111
 CC DB 82 LTAIAHCGKPLWAVGDHILLQ-GQRRTTRTSVVPKTHQGSPILPPLRTBDHDLML 140
 CC Qy 112 LRLRLPLPVYTSSYQPLPLNDCATAGTCHVSGMGITNHPRNPDPDIIQCLNLSIVSHAT 171
 CC DB 141 LKLARPVYPGPYRTRALQPLPYRCAQPDCOVAQNGTARRVYNGTJCSSITLSPKE 200
 CC Qy 172 CHGVYGRITSNNVAGGVPQGDAQCDGGPLVYCCGVLQGLVSWGSPCGDGIGPVY 231
 CC DB 201 CIEVFYPGVTTNNMCAGLDRGQPCDSGGPLVCDTQLGUSWG-VXPCCGSAQHPAVY 259
 CC Qy 232 TYCKYDVWIRMMRN 248
 CC DB 260 TQICKYMSWINKVIRSN 276
 CC RESULT 15
 CC ID TRY2_XENLA STANDARD; PRT; 244 AA.
 CC AC P70059;
 CC DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2003 (Rel. 4, Last annotation update)
 DB Trypsin precursor (BC 3.4.21.4).
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Xenopodidae; Xenopus.
 OC NCBITaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang K., Lytle L., Gan L., Hood L.B.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
 CC -|- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|>xaa, Lys-|>xaa.
 CC -|- CAPACTOR: Binds 1 calcium in per subunit (By similarity).
 CC -|- SUBCELLULAR LOCATION: Extracellular.
 CC -|- SIMILARITY: Belongs to peptidase family S1.
 CC
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 CC
 DR EMBL; U72310; RAB17274.1; -
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01-258;
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHMOTRYPAIN.
 DR PROSITE; SM00020; TRYPC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Digestion; Zymogen; Calcium-binding;
 KW Signal; Multigene family.
 FT SIGNAL 1 15
 FT PROPEP 16 21
 FT CHAIN 22 244
 FT ACT_SITE 61 61
 FT METAL 73 73
 FT METAL 75 75
 FT SIGNAL 1 15
 FT ACT_SITE 105 105
 FT DISULPID 198 198
 FT DISULPID 28 158
 FT DISULPID 46 62
 FT DISULPID 130 231
 FT DISULPID 137 204
 FT DISULPID 169 183
 FT DISULPID 194 218
 FT SITE 192 192
 SQ SEQUENCE 244 AP; 26079 MW; C63F29CB330B323 CRC64;

Query Match Score 41.0%; Score 563; DB 1; Length 244;
 Best Local Similarity 45.0%; Pred. No. 3.5e-39; Mismatches 8; Indels 8; Gaps 5;
 Matches 112; Conservative 46; Mismatches 83;

Qy 3 LS1FLIUCVGLSOA--ATPKIENGTBCGRNSOPWQCLPPESTSLRCGVVLDHRRVYTA 60
 Db 1 MRKPLVILVGLAVAFENDDKLYGGFTCAKNAVPYQTSNAGYHF-CGGSLSINSONVVA 59
 Qy 61 AHSGGSRWRVLLGEBHLSQLDWTBQIRHSFGSVTHPLGASTSHEDLRLRLRPVRV 120
 Db 60 AHGCKRSRQVLGEFEHNILNLNEGTEQFQINSQKVTKHPNY-NSRNLNDIMLKLSTPRL 117
 Qy 121 TSSVQPLPLPNDCATAGTECHYSGWGITHPRNPFPDOLQCLNLSTVHATCHGYGRI 180
 Db 118 SANIQSYLPSACASAGTNCISGWGNLSSCTNPDLOCLNAPLTDOSCSNSTYGBI 177

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Om protein - protein search, using sw model

Run on: June 16, 2004, 15:02:10 ; Search time 45 Seconds (without alignments)

Title: US-10-006-116A-194

Perfect score: 1374

Sequence: I MGLSISFLILUCVGLSQATP GVVTVICKYDWRIMMRNN 248

Scoring table: BL0SUM62

Gapext 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRNBL 25+*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacterioplasm:*

17: sp_archeap:*

Q9CPN9 mus musculu
O54B54 rattus norv
Q8NS59 homo sapien

Q9CPN7 mus musculu
Q91ve3 mus musculu
Q9r077 mus musculu
Q7te42 mus musculu
Q9zr9 mus musculu
Q9qk9 mus musculu
Q987H0 engraulis ja
Q8gpm3 argnilla ja
Q7TIR8 pangasius h
Q61275 rattus norv
Q8av83 brachydanio
Q9N1Q1 sequinus oe
Q99e00 mus musculu
Q29474 caris famili

Q9w7q6 paralichthys
Q8av11 oncorhynchus
Q63274 rattus norv
Q9w7q7 paralichthys

Q29474 caris famili
Q9W7Q6 petromyzon
Q7Bx90 brachydanio
Q92046 diabolichthys
Q8iu55 homo sapien
Q98599 notothenia

Q98599 engraulis ja
Q91515 fugu rubrip

ALIGNMENTS

RESULT 1	ID	Q9CV76	PRELIMINARY;	PRT;	234 AA.
	AC	Q9CV76			
	DT	01-JUN-2001 (TREMBlrel. 17, Created)			
	DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)			
	DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
	DB	2310008B01RIK protein (Fragment).			
	GN	2310008B01RIK.			
	OS	Mus musculus (Mouse).			
	OC	Buxtorveta; Meizoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	NCBI_TaxID	10090;			
	RN	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN=C57BL/6J; TISSUE=Tongue;			
	RX	MEDLINE=2108560; PubMed=11217851;			
	RA	Kawai J., Shinagawa A., Shibata M., Yoshino M., Itoh M., Ishii Y.,			
	RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
	RA	Aizawa K., Iwasa M., Niishi K., Kiyoosawa H., Kondo S., Yamanaoka I.,			
	RA	Saito T., Okada Y., Gotohori T., Bono H., de Bonaldo M.P.,			
	RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Saito R.,			
	RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
	RA	Kuel P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,			
	RA	Schirimi L.M., Staabli P., Suruki R., Tomita M., Wagner L., Washio T.,			
	RA	Sakai K., Okido T., Furuno M., Arai H., Baldarelli R., Barsh G.,			
	RA	Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.P.,			
	RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,			
	RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
	RA	Lyon P., Marchionni L., Mashima J., Mazzarulli J., Montabert P.,			
	RA	Nordone P., Rang B., Rodriguez I., Sakamoto N., Ringwald M.,			
	RA	Sakai K., Sato K., Schenckbach C., Seya T., Shiba Y., Storch K.-P.,			
	RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Wilming L.,			
	RA	Wynshaw-Boris A., Yoshida K., Hassegawa Y., Kawaji H., Kohtsuki S.,			
	RA	Hayashizaki Y.;			
	RT	"Functional annotation of a full-length mouse cDNA collection."			
	RL	Nature 409: 685-690 (2000).			
	CC	-1- SIMILARITY: BELONGS TO PBPTIDASE FAMILY S1.			
	DR	EMBL; AK009217; BAB26143.1; -.			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	952.5	69.3	234	11	Q9CV76		Q9CV76 mus mmusculi
2	627.5	45.7	260	4	Q8IW69		Q8iw69 homo sapien
3	608	44.3	254	11	Q8CCR4		Q8ccr4 mus mmusculi
4	601	43.7	275	4	Q8IXD7		Q8ixd7 homo sapien
5	597.5	43.5	249	11	Q9OYN4		Q9oyn4 mus mmusculi
6	597.5	43.5	276	11	Q9QVN3		Q9qvn3 m hippocastanum
7	588.5	43.3	255	4	Q96RQ0		Q96rq0 homo sapien
8	588.5	42.8	293	11	Q9D140		Q9d140 mus mmusculi
9	588	42.8	276	11	Q8CGR6		Q8cgr6 mus mmusculi
10	586	42.6	250	11	Q8CGRS		Q8cgrs mus mmusculi
11	578	42.1	242	11	Q8VS4		Q8vs4 mus mmusculi
12	563	41.0	248	13	Q7SZT1		Q7szt1 xenopus laevis
13	555	40.4	243	11	Q7S206		Q7s206 xenopus laevis
14	553.5	40.3	246	11	Q8B301		Q8b301 mus mmusculi
15	553.5	40.3	253	11	Q9IY82		Q9iy82 mus mmusculi
16	550.5	40.1	247	11	Q9D7Y7		Q9d7y7 mus mmusculi

DR	HSSP; P00763; 1DFO.	Query Match	Score 627.5;	DB 4;
DR	MEROPS; S01_020; -	Best Local Similarity	45.7%;	Pred. No. 1..4e-52;
DR	MDG; MGI:191676; -	Matches 123; Conservative	50.2%;	Mismatches 93; Indels 5; Gaps 3;
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.	Qy	5 IFILL---CVGLISQATPKIIFNGTBCGRNSOPWQVQLPFGTSLRCCGVLDHRWLTAA 61	
DR	GO; GO:0008233; F:peptidase activity; IEA.	Db	13 MFLLLGGAWAGHSRAQEDKVUGGBCOPHSQPWQAALPGQQQLCCGVLVGENWLTAA 72	
DR	GO; GO:0004295; F:trypsin activity; IEA.	Qy	62 HCSGSRYTWVLGEHLSQLDWYBQIRHSGGFSTWHPYLCAST-SHEIDLRLRRLPLPVV 120	
DR	InterPro; IPR00580; P:proteolysis and peptidolysis; IEA.	Db	73 HKKPKTVLRLDHSLSLQNDGPBEIIPVQSIPHPCYNSDVBDANNDMLQLRDQASL 132	
DR	InterPro; IPR001254; Peptidase_S1.	Qy	121 TSSVQPLPLPNDCATAGTCBVSGWGITNHPNPFPDOLQCLNLSTVSHATCHGVYPSRI 180	
DR	Pfam; PF00089; trypsin; 1.	Db	133 GSKVKPISLADICTOPEQKCTVSGWGVTSPPRENFPTILNCAEVKICPQQKRCBDAVPOI 192	
DR	PRINTS; PRO0022; CHYMOTRYPSIN.	Qy	181 TSNNMVCAGGEVPGQDAGCGDSCGPVLCGGVNLQCLVSNSVGPGCQDG1PGNTYICKVDN 240	
DR	SMART; SM00020; TRYPSIN_D1.	Db	193 TDVMCAGSSKGAEATCQGDSCGPVLCGALQITNSS-DPGCRSDPKGVTNCRYLDW 251	
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	KW Hydrolase; Pro tease; Serine protease.			
FT	NON_TER.			
FT	SEQUENCE 234 AA; 25888 MW; 6D81B6; 09EDD39110 CRC64;			
SQ				
<hr/>				
DR	Query Match	Score 952.5;	DB 11;	Length 234;
DR	Best Local Similarity	70.61;	Pred. No. 4..1e-84;	
DR	Matches 166; Conservative	27;	Mismatches 41; Indels 1; Gaps 1;	
Qy	14 LSQLQATPKIIFNGTBCGRNSOPWQVQLPFGTSLRCCGVLDHRWLTAAHCSSRTWVLG 73	Qy	241 IRMM 245	
Db	1 LSQADRKLYNGTECVRSNSQPVQVGLFTRKGVLTAAHCR-DKTVRLG 59	Db	252 IKKI 256	
RESULT 3				
DR	Q8CGR4 PRELIMINARY; PRT; 254 AA.			
Qy	74 EHSLSOLDWTEOIRHSGFSVTHPGTYLQASTSHEHDRLRLRRLPLPVVTSVPLPNDC 133	ID	Q8CGR4	
Db	60 EHSLSKLWDWTBQURHTTSRTPSYQAYQNTEHDRLRLRNLNPHTTRAVPVALPSNC 119	AC	Q8CGR4;	
Qy	134 ATAGTCBVSGWGTNHPRNPDPDILQCLNLSTIVSHATCHGYPGRTISNNWCAGGYPGQ 193	DT	01-MAR-2003 (TREMBLrel. 23; Created)	
Db	120 VTTGAMCHVSGCMTNTKRPWDPEPDRLQCLNLSTVSNETCRAVPGRVTEVNLCAGGBACK 179	DT	01-MAR-2003 (TREMBLrel. 23; Last sequence update)	
Qy	194 DACQGDSSGPGPLVGGVLOGLVWSGSVCPGDDG1PGVYTYICKVDRMIMRANN 248	DT	01-OCT-2003 (TREMBLrel. 25; Last annotation update)	
Db	180 DACQGDSSGPGPLVGGVNTQGLVWSGSVCPGQKG1PGVYTYICKVDTWIRVTRNN 234	DS	DBN KLK15.	
<hr/>				
DR	SEQUENCE FROM N.A.	RN	Mus musculus (Mouse)	
RP	MEDLINE=22325464; PubMed=12437987;	RX	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
RA	Ollison A.Y.; Lundwall A.	RA	OC Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RT	"Organization and evolution of the glandular kallikrein locus in Mus	RT	OC	
RL	muscarius".	RN	NCBI_TaxID=10090; NCBITaxonID=10090;	
RN	SEQUENCE FROM N.A.	RN	NCBI_TaxID=10090;	
RP	Submitted (SEB-2002) to the EMBL/GenBank/DBJ databases.	RP	SEQUENCE FROM N.A.	
RA	Adams M., Murai R.;	RA	SEQUENCE FROM N.A.	
RL	Submitted (SEB-2002) to the EMBL/GenBank/DBJ databases.	RL	Submitted (SEB-2002) to the EMBL/GenBank/DBJ databases.	
DR	MGD; MGI:2447533; XIK15.	DR	MGD; MGI:2447533; XIK15.	
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.	DR	GO; GO:0004263; F:chymotrypsin activity; IEA.	
DR	SMART; SM00020; TRYPSIN DOM; 1.	DR	SMART; SM00020; TRYPSIN DOM; 1.	
DR	PROST/TB; PS050240; TRYPSIN HIS; 1.	DR	PROST/TB; PS050240; TRYPSIN HIS; 1.	
DR	PROSITE; PS00134; TRYPSIN SER; 1.	DR	PROSITE; PS00134; TRYPSIN SER; 1.	
DR	PROSITE; PS00155; TRYPSIN SER; 1.	DR	PROSITE; PS00155; TRYPSIN SER; 1.	
DR	SEQUENCE 254 AA; 28042 MW; AA9328BBDD001861 CRC64;	SQ	SEQUENCE 254 AA; 28042 MW; AA9328BBDD001861 CRC64;	
<hr/>				
DR	Query Match	Score 608;	DB 11;	Length 254;
DR	Best Local Similarity	44.3%;	Pred. No. 1e-50;	
DR	Matches 124; Conservative	49.0%;	Mismatches 77; Indels 22; Gaps 7;	
Qy	5 IFILLCVLGISQAT--PKIPIGNGTBCGRNSOPWQVQLPFGTSLRCCGVLDHRWLTAA 62			
Db	1 MMILLAFULLVLSAQDCKVLEGEBCYPHSQPWQVALFERGERFNCGAFLSPRWLTAA 60			

Qy	63 CCGSRYWVRLGEHSLSQDWTQEIRHSGFSVTHPGYLCASTSHEHDILRLRLLPVRVTS	122	Qy	215 SWGSVGPCCQDGIPGVVTTICKYKVWDWIRMMRNN	248
Db	61 CCTRFMRVRLGEHNLRKTGPEQURSVRSLIPIFGY--EARTHFRHDIMLRLFLKPAULTA	118	Db	243 SWGS-DECAATRKGATVTRKVKYVDWICERMANN	275
Qy	123 SVQPLPLPNDCATAGTECHVSGMGITHNPRNP-----FPDLIQCLNTSIVSHAT 171				
Db	119 YVRPVALPRCPLIGEDCVSGHLLS-DANNPAGTGSOKSHVLPDTLHCANISIISEAS	177	RESULT 5		
Qy	172 CHGVTYGRITTSNNVCA---GGVPGSQDAGCGDSCGPVLYGVSNGVYGLVSYGCGQDQCP 228		09QYN4	PRELIMINARY;	PRT; 249 AA.
Db	178 CINQDGRVLPNVCAVGGG-GTDSCTGSDSPLVCOGALGIVSGDV-PCDTTRKRP 234		ID Q9QYN4;		
Qy	229 GVVYICKVWDWI 241		AC Q9QYN4;		
Db	235 GVVTKVCSYLEWI 247		RA 01-MAY-2000 (TREMBLrel.	13; Last sequence update)	
			DT 01-MAY-2000 (TREMBLrel.	13; Last annotation update)	
			DT 01-OCT-2003 (TREMBLrel.	13; Last annotation update)	
			DE HIPPOstasin.		
			GN PRSS20.		
			OS Mus musculus (Mouse).		
			OC Fukuyoya; Chordata; Craniata; Vertebrata; Euteleostomi;		
			OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
			NCBI_TaxID=10090;		
			[1]		
			RN RP SEQUENCE FROM N.A.		
			RC TISSUE=Brain;		
			RA Yamaguchi N.; Mitui S.;		
			RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
			[2]		
			RN RP SEQUENCE FROM N.A.		
			RC TISSUE=Brain;		
			RA Mitsu S.; Yamaguchi N.;		
			RT "cDNA cloning of a novel brain serine protease, Hippotasin."		
			RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.		
			DR EMBL; AB016226; BAA88825;1; --.		
			DR HSSP; P00763; 1DPO.		
			DR MROPS; S01_257; -.		
			DR MGDB; MGJ1929977; PRSS20.		
			DR GO; GO:0005576; C: extracellular; IDA.		
			DR InterPro; IPR009003; Cys_Ser_trypsin.		
			DR InterPro; IPR01554; Peptidase_S1.		
			DR InterPro; IPR01314; Peptidase_S1A.		
			DR Pfam; PF00089; trypsin_1.		
			DR PRINTS; PRO0122; CHYMOTRYPSIN.		
			DR SMART; SM00020; TRYSPC; 1.		
			DR DR PROSITE; PS00240; TRYPSIN_DOM; 1.		
			DR DR PROSITE; PS00134; TRYPSIN_HIS; 1.		
			DR DR PROSITE; PS00135; TRYPSIN_SER; 1.		
			SQ SEQUENCE 249 AA; E9FP9CB457D727D5 CRC64;		
			Query Match 43.5%; Score 597.5; DB 11; Length 249;		
			Best Local Similarity 47.0%; Pred. No. 1..1e-49;		
			Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;		
Qy	1 MGISTIPLLCVGLTSQATPKTPKNGTRCGRSNSQWQGLPFEGTSLRCGEVILDHRRWLLTA 60		Qy 1 MGISTIPLLCVGLTSQATPKTPKNGTRCGRSNSQWQGLPFEGTSLRCGEVILDHRRWLLTA 59		
Db	1 MIRLIALALVTHVGGT-RIKGYBKRPHSQWQVALFQTRLCLGATLIAPKWLLTA 59		Db 1 AHCGGSRTRVRLGEHSLSQDWTQEIRHSGFSVTHPGYLA--STSHEDRLRLLRLPV 118		
Qy	61 AHCGGSRTRVRLGEHSLSQDWTQEIRHSGFSVTHPGYLA--STSHEDRLRLLRLPV		Db 60 AHCRKPHVYHNLBTGDCEQRMRMATESPSPIDFNSLPNPKDHRNDIMLVMSPPV 119		
Db	60 AHCRKPHVYHNLBTGDCEQRMRMATESPSPIDFNSLPNPKDHRNDIMLVMSPPV		Qy 119 RVTSNSVQPLPNDICATGTCRVSGKGTINHPNPFPDLOQTLNSIYHATCHGIVPG 178		
Qy	119 RVTSNSVQPLPNDICATGTCRVSGKGTINHPNPFPDLOQTLNSIYHATCHGIVPG		Db 120 PPTAVQPTLSPHCAACTSCLISGWGTSSPOLRPHSLRCANVSIIBHKCECKAYPG 179		
Db	120 PPTAVQPTLSPHCAACTSCLISGWGTSSPOLRPHSLRCANVSIIBHKCECKAYPG		Qy 179 RITSNMVCG-GVYGQDQACQGDSCGSPVLCGGVLOGVSMGSVGPGQGDGAPGVYTYICKY 237		
Qy	179 RITSNMVCG-GVYGQDQACQGDSCGSPVLCGGVLOGVSMGSVGPGQGDGAPGVYTYICKY		Db 180 NTDTMLCASVRCREGKRDSCQGDSCPLVNGSLQGIIISMGQ-DPONTRKPGDVTVCY 238		
Db	180 NTDTMLCASVRCREGKRDSCQGDSCPLVNGSLQGIIISMGQ-DPONTRKPGDVTVCY		RESULT 6		
Qy	238 VDWIRMMRNN 248		Q9QYN3 PRELIMINARY;		
Db	239 FMTHEVMRNN 249		ID Q9QYN3		
Qy	156 PDLIQCLNTSIVSHATCHGTVGPRITSNVCAAG-GVPGGDACEQDSGGELVcevloqev 214				
Db	183 PHTLRCANTTIEHQKCNENAYPGNTIDTVCAVQBGKDSCQDSGGELVcnosLogII 242				

AC	Q9QXN3;	SEQUENCE FROM N.A.
DT	01-MAY-2000 (T-EMBLrel. 13; Created)	STRAIN=C57BL/6J; TISSUE=Tongue;
DT	01-MAY-2000 (T-EMBLrel. 13; Last sequence update)	MEDLINE=20530913; PubMed=11076861;
DT	01-OCT-2003 (T-EMBLrel. 25; Last annotation update)	RX
DE	Hippotaxisin prostate type. (Adult male tongue cDNA, RIKEN full-length enriched library, clone:331015108 product:protease; serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease; serine, 20, full insert sequence).	RA Konno H., Akiyama J., Nishi K., Kutsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA
OS	Mus musculus (Mouse)	RA
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	RA
OX	NCBI_TaxID=10090;	RA
RN	[1]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	Mitsui S., Okui A., Komimori K., Uemura H., Yamagushi N.; "CDNA cloning and tissue-specific splicing variants of mouse hippocasin/tLSP (PRSS20)." RIKEN full-length enriched library, clone:331015108 product:protease; serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease; serine, 20, full insert sequence).	RA Konno H., Akiyama J., Nishi K., Kutsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA
RA	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.	RA
RN	[2]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanasaki T., Harata A., Hayatsu N., Hiramoto K., Hirao T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kondo M., Koya S., Kuribara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibaoka K., Shihata Y., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T., Tera RA, Togawa Y., Yamamoto T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	RA Konno H., Akiyama J., Nishi K., Kutsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA
RN	[3]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanasaki T., Harata A., Hayatsu N., Hiramoto K., Hirao T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kondo M., Koya S., Kuribara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibaoka K., Shihata Y., Shiraki T., Tera RA, Togawa Y., Yamamoto T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	RA Konno H., Akiyama J., Nishi K., Kutsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA
RN	[4]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	The RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs." Nature 402:563-573 (2002).	RA Konno H., Akiyama J., Nishi K., Kutsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA
RN	[5]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"High-efficiency full-length cDNA cloning." Meth. Enzymol. 303:19-44 (1999).	RA Carninci P., Hayashizaki Y.; RA
RN	[6]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Functional annotation of a full-length mouse cDNA collection." Nature 409:685-690 (2001).	RA Carninci P., Hayashizaki Y.; RA
RN	[8]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes." Genome Res. 10:1617-1630 (2000).	RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; RA
RN	[1]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Riken integrated sequencing pipeline with 384 multicapillary sequencer." Genome Res. 10:1757-1771 (2000).	RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA
RN	[2]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[3]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[4]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[5]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[6]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[7]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[8]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[9]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[10]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[11]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[12]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[13]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[14]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[15]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[16]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[17]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[18]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[19]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[20]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[21]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[22]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[23]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[24]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[25]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[26]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[27]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[28]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[29]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[30]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[31]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[32]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[33]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[34]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[35]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[36]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[37]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[38]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[39]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[40]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[41]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[42]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[43]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[44]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[45]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[46]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[47]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[48]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[49]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[50]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.; RA
RN	[51]	RA
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;	STRAIN=C57BL/6J; TISSUE=Tongue;
RA	"Peptidase family S1." Mamm. Genome Res. 10:1757-1771 (2000).	RA Carninci P., Hayashizaki Y.;

RESULT 9						
Q8CGR6	PRELIMINARY:	PRT:	276 AA.			
ID Q8CGR6						
AC Q8CGR6;						
DT 01-MAR-2003 (TREMBIEl. 23, Created)						
DT 01-MAR-2003 (TREMBIEl. 23, Last sequence update)						
DT 01-OCT-2003 (TREMBIEl. 25, Last annotation update)						
DB Glandular kallikrein KLKL3.						
GN KLKL3.						
OS Mus musculus (Mouse).						
OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.						
RN [1]	SEQUENCE FROM N.A.					
RP MEDLINE-22325984; PubMed-12437987;						
RA Olsbøn A.Y.; Lundwall A.;						
RA NCBI_TaxID=10090;						

Query Match	Score	DB ID	Length	Details
Best Local Similarity	42.1%	Score 578; DB 11;	Length 242;	
Matches 114;	Pred. No. 7.9e-48;			
Matches 35;	Mismatches 75;	Indels 8;	Gaps 5;	
Qy 21 KIFNGTECGRNSSOPWQVSLGFFECTSLR--CGVYLIDHRWLVTAHACGSRSRYWRLGEISLS 78	Score 563;	DB 13;	Length 248;	Query Match
15 KLGIGTRCVRSNQWPQVALAQAGFGRFLGGIVLSDQVITAAHCARPLHYALGKHNIR 74	Best Local Similarity 45.0%;	Pred. No. 2.3e-46;		Best Local Similarity
Qy 79 QDWTQEQRHSFSVTTHPGYLGASTSHEDILRLRIPVTTSSQPLPLPNDCATAGT 138	Matches 46;	Mismatches 83;	Indels 8;	Matches
75 RWEATQQYVRVARQPHFQY.-QPOAINDNDMLKLQKVKVLGRAVKTIVSASSCASEGT 132	112; Conservative			112; Conservative
Qy 139 ECHVSGMGTINHPRNPFPDLLOCNLNSIVSHATCHGTPGRITSNNMVAGGGP--GODAC 196	3 LSIFULLCIVGLSLSR-	ATPKIFNTBECGRNSOPMQVGLPEGTSLRQVLLDHRWLVTLA 60		Matches
Db 133 PERVSQGMGTIAPPIARYPTALQCUVNIMSEQAACHRAYPGITTSGMVCA-GVPEGGRDSC 191	5 MKPLVLVLUVGAAYAFDDDKRIVGGTCAKANAVPOVSLNAGYHF-CGSSLINSQTVVSA 63			5 MKPLVLVLUVGAAYAFDDDKRIVGGTCAKANAVPOVSLNAGYHF-CGSSLINSQTVVSA 63
Qy 197 QDGSQGPVLUCCGTVLOGIVSMGVPGPCGQDGIPGVYTYICKYDWRIMMRNN 248	61 AHCSGSRYSYTRLGHEISLSQLDTEQRHSGFSWTHPGYLGASTSHEDILRLRIPVTRV 120			61 AHCSGSRYSYTRLGHEISLSQLDTEQRHSGFSWTHPGYLGASTSHEDILRLRIPVTRV 120
Db 192 QDGSQGPVLUCCGTVLOGIVSMGVPGPCGQDGIPGVYTYICKYDWRIMMRNN 242	64 AHCYKSRIQYRGLGEENITAIALNEGTEQFDISQVKHPPN--NSRNLDNDIMPLKLSTTARL 121			64 AHCYKSRIQYRGLGEENITAIALNEGTEQFDISQVKHPPN--NSRNLDNDIMPLKLSTTARL 121
Qy 121 TSSVQPLPNDPDCATAGTECHVSGMGTINHPRNPFPDLLOCNLNSIVSHATCHGTPGRIGRI 180	Qy 61 TSSVQPLPNDPDCATAGTECHVSGMGTINHPRNPFPDLLOCNLNSIVSHATCHGTPGRIGRI 180			Qy 61 TSSVQPLPNDPDCATAGTECHVSGMGTINHPRNPFPDLLOCNLNSIVSHATCHGTPGRIGRI 180
Db 122 SANIQSVPLPSACASAGTNCIUSGNTLSSGNTYFPLDQCLNAPLTDSQNSNPGBI 181	Qy 122 SANIQSVPLPSACASAGTNCIUSGNTLSSGNTYFPLDQCLNAPLTDSQNSNPGBI 181			Db 122 SANIQSVPLPSACASAGTNCIUSGNTLSSGNTYFPLDQCLNAPLTDSQNSNPGBI 181
Qy 181 TSNMVCAGGYP-GODACOGDGGPLVCGGYLQGLYWSVGSPCGQDGIPGVYTYICKYDWRIMMRNN 239	Qy 181 TSNMVCAGGYP-GODACOGDGGPLVCGGYLQGLYWSVGSPCGQDGIPGVYTYICKYDWRIMMRNN 239			Qy 181 TSNMVCAGGYP-GODACOGDGGPLVCGGYLQGLYWSVGSPCGQDGIPGVYTYICKYDWRIMMRNN 239
Db 182 TKNMFAGFLAGGDSQGDGGPvRCGDSQGDGGPvRCGDSQGDGGPvRCGDSQGDGGPvRCNFVU 239	Db 182 TKNMFAGFLAGGDSQGDGGPvRCGDSQGDGGPvRCGDSQGDGGPvRCGDSQGDGGPvRCNFVU 239			Db 182 TKNMFAGFLAGGDSQGDGGPvRCGDSQGDGGPvRCGDSQGDGGPvRCGDSQGDGGPvRCNFVU 239
RESULT 12				
Q7SZT1 PRELIMINARY;	PRT;	248 AA.		
ID Q7SZT1;				Qy 240 WIRNMIRNN 248
AC Q7SZT1;				Db 240 WIQSTISSN 248
DT 01-OCT-2003 (TREMBLrel. 25, Created)				
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)				
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE TRYPSIN (Fragment).				
OS Xenopus laevis (African clawed frog).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;				
Xenopodinae; Xenopus.				
NCBI_TaxID:8355;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE=Spleen;				
RX MEDLINE=22341132; PubMed=12454917;				
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,				
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,				
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative." Dev. Dyn. 225:384-391 (2002).				
RT Dev. Dyn. 225:384-391 (2002).				
RL RN [1]				
RN SEQUENCE FROM N.A.				
RC TISSUE=Spleen;				
RX MEDLINE=22341132; PubMed=12454917;				
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Hopkins R.P., Jordan H., Moore T., Max S.I., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R., Brownstein M.J., Usdin T.B., Yoshiaki S., Prange C., Blakesley R.W., Touchman J.W., Green E.D., McEvlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibb R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smilus D.E., Schnierch A., Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				
RT SEQUENCE FROM N.A.				
RA Klein S., Strausberg R.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Submitted to the EMBL/GenBank/DBJ databases.				
RC TISSUE=Spleen;				
RX MEDLINE=22341132; PubMed=12454917;				
RA Blakesley R.W., Touchman J.W., Green E.D., Schmutz J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Scherf A., Schein J.B., Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Submitted to the EMBL/GenBank/DBJ databases.				
RT RT				

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[3] SEQUENCE FROM N.A.

RP TISSUE=Whole;

RC Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RA Klein S., Strausberg R.;

DR Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

KW Hypothetical protein; AAU54194; AAU54194.1; -.

SQ SEQUENCE 243 AA; 25476 MW; C5BB2B450B209F31 CRC64;

Query Match 40.4%; Score 555; DB 13; Length 243;

Best Local Similarity 45.7%; Pred. No. 1..3e-45;

Matches 113; Conservative 42; Mismatches 82; Indels 10; Gaps 6;

Qy 6 FLLLCVGLSQQAT--PKIFNGTGCGRNSOPWQVGLPFGTSILRGCVNLIDHRYVLTAAH 62

Db 3 FLLLCVCL-LGAAAAPDDKLIGGATCAKSSVPYIYLNSQVHP-CGGSJUTNQVVAHH 60

Qy 63 CGSRVYWRUGBEHSLSQLDNTBQIRHSGFSVTHPGVLAESTSHEDRLRRLRPLPVRVTS 122

Db 61 CYKASTQVRLGEHTNALSGETBQPISSSKVTRHSGY-NSYTLDNDIMMLIKSSPASLNA 118

Qy 123 SVQPLPLNDCATAGTCBHYSGWGFTNHPRNPFPDQLQCLNLSTVSHATCHGVYGRITS 182

Db 119 AVNTVPLSGSAAGTCSLISGWGNTLNSGNSYPDQLCNAPIJNAQNSATPGEITA 178

Qy 183 NMVUAGGVP-GODACOGDSCGPVLYCCGVVQCLVWSNGSVPGQGDQGIPGTYTICKYVDWI 241

Db 179 NMICYGFMEEGRKDSCQDSCGPVYCNQGQzvsvsGy-SCAMRNYPGYTCKVNNAWT 236

Qy 242 RMIMRN 248

Db 237 QNTIAAN 243

RESULT 14

088301 PRELIMINARY; PRT; 246 AA.

AC 088301; 08-Nov-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Serine protease (BSP).

PRSS18 OR MBSP.

OS Mus musculus (Mouse).

OC Mecarao; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.

OX NCBI_TaxID=10090; [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Matsui H., Takahashi T.;

RT "Mouse serine protease preferentially expressed in brain.";

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL;

RA Matsui H., Takahashi T.;

RT "The sequences of mouse serine protease gene expressed in brain."

RL "A novel serine protease expressed in the hair follicle."

RT Submitted (FB-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RA Meier N., Dear T.N., Boehm T.;

RT "A novel serine protease expressed in the hair follicle."

RL Submitted (FB-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Matsui H., Takahashi T.;

RT "The sequences of mouse serine protease gene expressed in brain."

RL Submitted (SBP-1999) to the EMBL/GenBank/DBJ databases.

CC !- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; AB015206; BAA28895.1; -.

DR EMBL; Y18723; CAA77269.1; -.

DR EMBL; AB032402; BAA84544.1; -.

DR HSSP; P00753; IDPO.

DR MEROPS; S01-236; -.

MGD; MGI:1343166; PRSS18.

DR GO; GO:0004263; P:chymotrypsin activity; IBA.

DR GO; GO:0008233; P:peptidase activity; IBA.

DR GO; GO:004295; P:trypsin activity; IBA.

DR InterPro; IPRO009003; Cys Ser tryptase; IBA.

DR InterPro; IPRO01254; Peptidase_S1.

DR InterPro; IPRO01314; Peptidase_S1A.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00020; TRYSP; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS50033; TRYPSIN_HIS; 1.

DR PROSITE; PS00335; TRYPSIN_SRR; 1.

KW Hydrolase; Protease; Serine protease.

SEQUENCE 246 AA; 27496 MW; E20C080087119B63 CRC64;

SQ Query Match 40.3%; Score 553.5; DB 11; Length 246;

Best Local Similarity 43.5%; Pred. No. 1..9e-45;

Matches 107; Conservative 46; Mismatches 82; Indels 8 11; Gaps 6;

Qy 7 LLLCVIGLSQAA---TPKLENGTECGRNSOPWQVGLPEGSTSLRGGVLIIDHRWVLTAAH 62

Db 4 LALCAAWSESEQKVHGGCLKDISHPFOAALYTSGHLLCGVLDQWVLTAAH 62

Qy 63 CGSSEYWRLGHSISQLDWTEQIRHSGPSVTHPGYLASTSHEDLRLRPLPVRTS 122

Db 63 CKKPQLQVILGRNKIRQETPQRQISVDTIVHPRY-NPETHNDIMMVHLKNPKFSK 120

Qy 123 SVQPLPLNDCATAGTCBHYSGWGFTNHPRNPFPDQLQCLNLSTVSHATCHGVYGRITS 182

Db 119 AVNTVPLSGSAAGTCSLISGWGNTLNSGNSYPDQLCNAPIJNAQNSATPGEITA 178

Qy 183 NMVUAGGVP-GODACOGDSCGPVLYCCGVVQCLVWSNGSVPGQGDQGIPGTYTICKYVDWI 241

Db 179 NMVCAAGGY-PGQDAGQDQGDSGPVLYGGVQGLYSWGSVPGCGQDQGIPGTYTICKYVDWI 237

Qy 183 NMVCAAGGY-PGQDAGQDQGDSGPVLYGGVQGLYSWGSVPGCGQDQGIPGTYTICKYVDWI 241

Db 179 NMVCAAGDY-PGQDAGQDQGDSGPVLYGGVQGLYSWGSVPGCGQDQGIPGTYTICKYVDWI 237

RESULT 15

Q91182 ID Q91182 PRELIMINARY; PRT; 253 AA.

AC 091182; 091182; PRELIMINARY; PRT; 253 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DR 00761; 1AN1; Neurosin (Protease, serine, 18).

GN PRSS18.

OS Mus musculus (Mouse).

OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090; [1]

RN SBQNUCE FROM N.A.

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Mitsui S., Yamaguchi N.;

RT "cDNA cloning and characterization of mouse brain specific serine

protease, Neurosin."

RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAUSBERG R.

RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; AB008928; BAA55605.1; -.

DR EMBL; BC011119; AAH31119.1; -.

DR HSSP; P00761; 1AN1.

DR MEROPS; S01-236; -.

DR MGD; MGI:1343166; PRSS18.

DR GO; GO:0004263; P:chymotrypsin activity; IBA.

DR GO; GO:0008233; P:peptidase activity; IBA.

DR GO; GO:004295; P:trypsin activity; IBA.

DR GO; GO:004295; P:trypsin activity; IBA.

```

DR GO; GO:0004295; Protein activity; IBA.
DR GO; GO:0006508; Proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Cys-Ser_trypsin.
DR InterPro; IPR001344; Peptidase_S1.
DR Pfam; PF0089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPIN.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HHS; 1.
DR PROSITE; PS00135; TRYPSIN_SRR; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE: 253 AA; 28329 MW; CSEF98C7B8P2PBC1 CRC64;

```

Query	Match	Score	Length	DB	Indels	Gaps
Qy	Best Local Similarity	40.3%	253	No.	2e-45;	
Qy	Matches 107; Conservative	43.5%	82;	Mismatches	11;	6;
Db	11 LALCIV-LAKSAWSEEQKRVHGGPCLKNSHPFQAALVTSGHLLCGVILIDECWVLTAHH	62				
Qy	63 CGSGRXYWRLGEHSISQDWTBQRHSGGSVTHRGYLGASTSHEDLRLRGLPVRVTS	122				
Db	70 CKKENLQLVILGRNHLRQTETFQRQISVDTIVHRY-NPETHNDIMMHLKNPVKPSK	127				
Qy	123 SYQPLPLPDPDCATAGTCVHSWGMGTNHRPNPPDILLOCNTSLTVSHATCHGTYPPGRITS	182				
Db	128 KIQPPPLKNDCSBERPNCCQLLGWG - KMENGDFPTDITQADVHLVPRECERAYPGKLTQ	185				
Qy	183 NMVCAAGGV-PGQDACAQGDSGGPLVYGGCVLQGIVSWGSVGPMSGDGIPGSYTYICKYDWI	241				
Db	186 SMVCAAGDMEEGNDSCQDSCGPLYCGGRRLQVSWGDM PCGSKEKGTYTDCTHIRWI	244				
Qy	242 RMIRRN 247					
Db	245 QNLRN 250					

Search completed: June 16, 2004, 15:06:19
 Job time : 47 secs

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Om protein - protein search, using sw model

Run on: June 16, 2004, 15:06:56 ; Search time 60 Seconds (without alignments)

total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqP1980s:*
- 2: geneseqP1990s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003s:*
- 7: geneseqP2003s:*
- 8: geneseqP2004s:*

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Title:	US-10-006-116A-194
Perfect score:	248
Sequence:	1 MGLSIPFLCVLGIQSQATP GVVYVICKYDWRIMMRNN 248
Scoring table:	Oligo Gapop 60.0 , Gapext 60.0
Searched:	1586107 seqs, 282547505 residues
Word size :	0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqP1980s:*
- 2: geneseqP1990s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003s:*
- 7: geneseqP2003s:*
- 8: geneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	248	100.0	248	3	AAB21304	Aab21304	Human KLK
2	248	100.0	248	3	AAB24428	Aab24428	Human PRO
3	248	100.0	248	3	AAB24032	Aab24032	Human PRO
4	248	100.0	248	3	AY939393	Aay939393	Human PRO
5	248	100.0	248	4	AAM23994	Aam23994	Human EST
6	248	100.0	248	4	AAB66142	Aab66142	Protein O
7	248	100.0	248	6	Abo33635	Abo33635	Novel hum
8	248	100.0	248	7	ABo44488	Abo44488	Human sec
9	248	100.0	248	7	ABo33512	Abo33512	Novel hum
10	248	100.0	248	7	ADC18063	Adc18063	Human PRO
11	248	100.0	248	7	ADD70709	Add70709	Human sec
12	248	100.0	248	7	ADD39786	Add39786	Human sec
13	248	100.0	248	7	ADD70232	Add70232	Human sec
14	248	100.0	248	7	ADD38353	Add38353	Human sec
15	248	100.0	248	7	ADD39109	Add39109	Human sec
16	248	100.0	248	7	ADD38832	Add38832	Human sec
17	248	100.0	248	7	ADD40263	Add40263	Human sec
18	248	100.0	248	7	ADDS0484	Ado30484	Human sec
19	248	100.0	248	7	ADB20096	Adb20096	Human sec
20	248	100.0	248	7	ADB50007	Adb50007	Human sec
21	248	100.0	248	7	ADE21565	Ade21565	Human sec
22	235	94.8	254	3	AAB21303	Aab21303	Human KLK
23	235	94.8	254	5	ABG66676	Abg66676	Human nov
24	184	74.2	184	3	AAB21301	Aab21301	Human KLK
25	184	73.4	248	6	Aao29516	Aao29516	Human kal

The present sequence is one of four alternatively spliced kalikrein-like proteins encoded by the human KLK-L4 gene. Kalikreins and kalikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kalikrein-like proteins KLK-L1, KLK-L2, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used

RESULT 1							
ID	AAAB1304	standard; Protein;	248 AA.	XX	AC	XX	XX
DT	02-FEB-2001	(first entry)		XX			
DE	Human KLK-L5	Protein #4.		XX			
KW	Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6; kalikrein-like protein; serine protease; cytosstatic; cancer; prostate cancer.			XX			
OS	Homo sapiens.			XX			
PN	W0200053776-A2.			XX			
PD	14-SEP-2000.			XX			
PP	09-MAR-2000; 2000000-CA000258.			XX			
PR	11-MAR-1999; 99US-0124260P.			PR	01-APR-1999; 99US-012386P.		
PR	21-JUL-1999; 99US-014419P.			XX			
PA	(M001N) MOUNT SINAI HOSPITAL.			XX			
PI	Youcef GM, Diamandis EP;			XX			
DR	WPI; 2000-587440/55.			XX			
DR	N-PSDB; AAA9944.			XX			
PT	New kalikrein-like (KLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.			XX			
PS	Claim 12; Page 172; 184pp; English.			XX			

CC to treat conditions mediated by the kallikrein-like proteins
 XX Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182; Mismatches 0; Indels 0; Gaps 0;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSIPILPLCIVGLSQATPKLIFNGTEGRNSQPMQVGLFEGTSIARCGVLLIDHRWVLTAA 60

Db 1 MGLSIPILPLCIVGLSQATPKLIFNGTEGRNSQPMQVGLFEGTSIARCGVLLIDHRWVLTAA 60

Qy 61 AHCGSGRXYWRVGEHSLSQLDWTEQIRHSQFSYTHRCGASTSHEDHLRLRLRLPVRV 120

Db 61 AHCGSGRXYWRVGEHSLSQLDWTEQIRHSQFSYTHRCGASTSHEDHLRLRLRLPVRV 120

Qy 121 TSSVQPLPLNDCATACTECHVSGWGTINHPRNPPDQLQCLNLSIVSHATCHGTYGPGR 180

Db 121 TSSVQPLPLNDCATACTECHVSGWGTINHPRNPPDQLQCLNLSIVSHATCHGTYGPGR 180

Qy 181 TSNMVCAAGVPEQDACCSDGSPPLVCEGVVQLOGLVSNSVGPGQDQDIPGTTYICKYVDW 240

Db 181 TSNMVCAAGVPEQDACCSDGSPPLVCEGVVQLOGLVSNSVGPGQDQDIPGTTYICKYVDW 240

Qy 241 IRMIMRN 248

Db 241 IRMIMRN 248

RESULT 2
 AAB24428
 ID AAB24428 standard; protein; 248 AA.
 XX AC AAB24428;
 XX DT 07-NOV-2000 (first entry)
 DE Human PRO1303 protein sequence SEQ ID NO:203.

XX Human; PRO: promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma; wound; cancer; atherosclerosis; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine.
 XX Homo sapiens.
 XX PN WO200032221-A2.
 XX PD 08-JUN-2000.
 XX PF 30-NOV-1999; 99WO-US028313.
 XX PR 01-DEC-1998; 99WO-US02510B.
 PR 16-DEC-1998; 99US-012850B.
 PR 08-MAR-1999; 99US-011555B.
 PR 08-MAR-1999; 99WO-US00503B.
 PR 12-MAR-1999; 99US-0123957B.
 PR 12-MAR-1999; 99US-0131445B.
 PR 14-MAY-1999; 99US-0134287B.
 PR 02-JUN-1999; 99WO-US012224.
 PR 23-JUN-1999; 99US-0141037B.
 PR 20-JUL-1999; 99US-0144758B.
 PR 26-JUL-1999; 99US-014569B.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020534.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021030.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023039.
 PR 29-OCT-1999; 99US-0162508B.
 XX PA (GETH) GENENTECH INC.

CC to treat conditions mediated by the kallikrein-like proteins
 XX Sequence 248 AA;
 Query Match 100.0%; Score 248; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182; Mismatches 0; Indels 0; Gaps 0;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSIPILPLCIVGLSQATPKLIFNGTEGRNSQPMQVGLFEGTSIARCGVLLIDHRWVLTAA 60

Db 1 MGLSIPILPLCIVGLSQATPKLIFNGTEGRNSQPMQVGLFEGTSIARCGVLLIDHRWVLTAA 60

Qy 61 AHCGSGRXYWRVGEHSLSQLDWTEQIRHSQFSYTHRCGASTSHEDHLRLRLRLPVRV 120

Db 61 AHCGSGRXYWRVGEHSLSQLDWTEQIRHSQFSYTHRCGASTSHEDHLRLRLRLPVRV 120

Qy 121 TSSVQPLPLNDCATACTECHVSGWGTINHPRNPPDQLQCLNLSIVSHATCHGTYGPGR 180

Db 121 TSSVQPLPLNDCATACTECHVSGWGTINHPRNPPDQLQCLNLSIVSHATCHGTYGPGR 180

Qy 181 TSNMVCAAGVPEQDACCSDGSPPLVCEGVVQLOGLVSNSVGPGQDQDIPGTTYICKYVDW 240

Db 181 TSNMVCAAGVPEQDACCSDGSPPLVCEGVVQLOGLVSNSVGPGQDQDIPGTTYICKYVDW 240

Qy 241 IRMIMRN 248

Db 241 IRMIMRN 248

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182; Mismatches 0; Indels 0; Gaps 0;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSIPILPLCIVGLSQATPKLIFNGTEGRNSQPMQVGLFEGTSIARCGVLLIDHRWVLTAA 60

Db 1 MGLSIPILPLCIVGLSQATPKLIFNGTEGRNSQPMQVGLFEGTSIARCGVLLIDHRWVLTAA 60

Qy 61 AHCGSGRXYWRVGEHSLSQLDWTEQIRHSQFSYTHRCGASTSHEDHLRLRLRLPVRV 120

Db 61 AHCGSGRXYWRVGEHSLSQLDWTEQIRHSQFSYTHRCGASTSHEDHLRLRLRLPVRV 120

Qy 121 TSSVQPLPLNDCATACTECHVSGWGTINHPRNPPDQLQCLNLSIVSHATCHGTYGPGR 180

Db 121 TSSVQPLPLNDCATACTECHVSGWGTINHPRNPPDQLQCLNLSIVSHATCHGTYGPGR 180

Qy 181 TSNMVCAAGVPEQDACCSDGSPPLVCEGVVQLOGLVSNSVGPGQDQDIPGTTYICKYVDW 240

Db 181 TSNMVCAAGVPEQDACCSDGSPPLVCEGVVQLOGLVSNSVGPGQDQDIPGTTYICKYVDW 240

Qy 241 IRMIMRN 248

Db 241 IRMIMRN 248

XX RESULT 3
 AAB24432
 ID AAB24432 standard; protein; 248 AA.
 XX AC AAB24432;
 XX DT 25-JAN-2001 (first entry)
 DE Human PRO1303 protein sequence SEQ ID NO:33.
 XX KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumourigenesis; anticancer; detection.
 XX OS Homo sapiens.
 XX PN WO200053750-A1.
 XX PD 14-SBP-2000.

PR molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 12; Fig 10B; 773pp; English.

XX

PS XX

PS XX

PR 02-OCT-1998; 98US-0102571P.

PR 01-OCT-1998; 98US-0102681P.

PR 01-OCT-1998; 98US-0102681P.

PR 02-OCT-1998; 98US-0102963P.

PR 06-OCT-1998; 98US-0103258P.

PR 06-OCT-1998; 98US-0103443P.

PR 07-OCT-1998; 98US-0103311P.

PR 07-OCT-1998; 98US-0103311P.

PR 07-OCT-1998; 98US-0103328P.

PR 07-OCT-1998; 98US-0103328P.

PR 07-OCT-1998; 98US-0103399P.

PR 07-OCT-1998; 98US-0103399P.

PR 07-OCT-1998; 98US-0103403P.

PR 08-OCT-1998; 98US-0103633P.

PR 08-OCT-1998; 98US-0103679P.

PR 08-OCT-1998; 98US-0103679P.

PR 08-OCT-1998; 98US-0103711P.

PR 14-OCT-1998; 98US-0104257P.

PR 20-OCT-1998; 98US-0104987P.

PR 20-OCT-1998; 98US-0105000P.

PR 21-OCT-1998; 98US-0105104P.

PR 22-OCT-1998; 98US-0105163P.

PR 22-OCT-1998; 98US-0105266P.

PR 26-OCT-1998; 98US-0105693P.

PR 26-OCT-1998; 98US-0105693P.

PR 27-OCT-1998; 98US-0105807P.

PR 27-OCT-1998; 98US-0105889P.

PR 27-OCT-1998; 98US-0105889P.

PR 27-OCT-1998; 98US-0106027P.

PR 28-OCT-1998; 98US-0106022P.

PR 28-OCT-1998; 98US-0106022P.

PR 28-OCT-1998; 98US-0106030P.

PR 28-OCT-1998; 98US-0106032P.

PR 28-OCT-1998; 98US-0106033P.

PR 28-OCT-1998; 98US-0106034P.

PR 29-OCT-1998; 98US-0106241P.

PR 29-OCT-1998; 98US-0106384P.

PR 29-OCT-1998; 98US-0108505P.

PR 30-OCT-1998; 98US-0106464P.

PR 03-NOV-1998; 98US-0106551P.

PR 03-NOV-1998; 98US-0106902P.

PR 03-NOV-1998; 98US-0106902P.

PR 03-NOV-1998; 98US-0106913P.

PR 03-NOV-1998; 98US-0106913P.

PR 10-NOV-1998; 98US-0107783P.

PR 17-NOV-1998; 98US-0108775P.

PR 17-NOV-1998; 98US-0108779P.

PR 17-NOV-1998; 98US-0108787P.

PR 17-NOV-1998; 98US-0108788P.

PR 17-NOV-1998; 98US-0108801P.

PR 17-NOV-1998; 98US-0108801P.

PR 17-NOV-1998; 98US-0108848P.

PR 18-NOV-1998; 98US-0108848P.

PR 18-NOV-1998; 98US-0108850P.

PR 18-NOV-1998; 98US-0108850P.

PR 18-NOV-1998; 98US-0108851P.

PR 18-NOV-1998; 98US-0108852P.

PR 18-NOV-1998; 98US-0108852P.

PR 18-NOV-1998; 98US-0108904P.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker K., Goddard A., Gurney AL, Smith V., Watanabe CK, Wood WI;

XX

DR WPI: 2000-237871/20.

XX

PT New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small

PR molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 12; Fig 10B; 773pp; English.

CC AAA37022 to AAA37144 encode the new isolated human transmembrane receptor or secreted PRO polypeptides given in AAY9340 to AAY9462. The transmembrane and receptor or secreted PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding them have various industrial applications, including uses as pharmaceutical and diagnostic agents. AA337145 to AAA37310 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.

XX

SQ Sequence 248 AA:

Query	Match	Score	DB	Length
1 MGISIPIFLICVLGLSQATTPKIPNQTECGRNSOPWQVCLFEGTSLRCCGVLLIDHRWVLTAA	100.0%	248	DB 3: Pred. No. 8.4e-182;	100.0% Mismatches 0; Indels 0; Gaps 0;
1 MGISIPIFLICVLGLSQATTPKIPNQTECGRNSOPWQVCLFEGTSLRCCGVLLIDHRWVLTAA	100.0%	248	DB 1 Pred. No. 8.4e-182;	100.0% Mismatches 0; Indels 0; Gaps 0;
61 AHCGSGRYWWRGHSISQLDNTBQIRHSGPSVTHPGTLGASTSHADRLRLRLRPLPYR	120	61 AHCGSGRYWWRGHSISQLDNTBQIRHSGPSVTHPGTLGASTSHADRLRLRLRPLPYR	120	
61 AHCGSGRYWWRGHSISQLDNTBQIRHSGPSVTHPGTLGASTSHADRLRLRLRPLPYR	120	61 AHCGSGRYWWRGHSISQLDNTBQIRHSGPSVTHPGTLGASTSHADRLRLRLRPLPYR	120	
121 TSSVQPLPLNDPDCATAGTCBHYSGMGITNHPRNPFPDQLQCLNTSIVSHATCHGVPYERI	180	121 TSSVQPLPLNDPDCATAGTCBHYSGMGITNHPRNPFPDQLQCLNTSIVSHATCHGVPYERI	180	
121 TSSVQPLPLNDPDCATAGTCBHYSGMGITNHPRNPFPDQLQCLNTSIVSHATCHGVPYERI	180	121 TSSVQPLPLNDPDCATAGTCBHYSGMGITNHPRNPFPDQLQCLNTSIVSHATCHGVPYERI	180	
181 TSMMVAGGVPQGQDACCQDSGGPLVCGSYLQVSHGSVVGPCQDGIPGVYTICKYDN	240	181 TSMMVAGGVPQGQDACCQDSGGPLVCGSYLQVSHGSVVGPCQDGIPGVYTICKYDN	240	
181 TSMMVAGGVPQGQDACCQDSGGPLVCGSYLQVSHGSVVGPCQDGIPGVYTICKYDN	240	181 TSMMVAGGVPQGQDACCQDSGGPLVCGSYLQVSHGSVVGPCQDGIPGVYTICKYDN	240	
241 IRMINMRIN 248	241 IRMINMRIN 248	241 IRMINMRIN 248	241 IRMINMRIN 248	
241 IRMINMRIN 248	241 IRMINMRIN 248	241 IRMINMRIN 248	241 IRMINMRIN 248	

RESULT 5

ID AAM23994 standard; protein; 248 AA.

XX

XX AAM23994;

XX AC AAM23994;

XX 12-OCT-2001 (first entry)

DE Human EST encoded protein SEQ ID NO: 1519.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; BST; diagnostics; forensics test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.

XX Homo sapiens.

OS XX

XX WO200154477-A2.

XX

XX 02-AUG-2001.

XX

XX 25-JAN-2001; 2001WO-US002687.

XX

XX PR 25-JAN-2000; 2000US-0049104.

XX PR 17-JUL-2000; 2000US-0061746.

XX PR 03-AUG-2000; 2000US-00631451.

XX PR 15-SEP-2000; 2000US-0063870.

XX

PA (HYSEQ INC.

XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Werzman T;

PI Cao Y, Dumanac RA, Zhang J, Werzman T;

PT

KW cartilage disorder; sports injury; arthritis.

XX 06-OCT-1998; 98US-0103258P.
 OS PR 06-OCT-1998; 98US-010349P.
 OS PR 07-OCT-1998; 98US-010314P.
 PN XX PR 07-OCT-1998; 98US-010315P.
 PN PR 07-OCT-1998; 98US-010328P.
 XX PR 07-OCT-1998; 98US-0103395P.
 PD PR 07-OCT-1998; 98US-0103396P.
 XX PR 07-OCT-1998; 98US-0103401P.
 PP PR 08-OCT-1998; 98US-0103533P.
 XX PR 08-OCT-1998; 98US-0103678P.
 PR PR 08-OCT-1998; 98US-0103679P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098811P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099538P.
 PR 09-SEP-1998; 98US-00995602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100394P.
 PR 16-SEP-1998; 98US-0100527P.
 PR 16-SEP-1998; 98US-0100561P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 18-SEP-1998; 98US-0100711P.
 PR 18-SEP-1998; 98US-0100919P.
 PR 22-SEP-1998; 98US-0100930P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 24-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102007P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 01-OCT-1998; 98US-0102644P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.

PPR	29-SBP-1998	98US-0102331P
PPR	30-SBP-1998	98US-0102484P.
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PPR	30-SBP-1998	98US-0102571P.
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PPR	02-OCT-1998	98US-0102695P.
PPR	02-OCT-1998	98US-0103258P.
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PPR	08-OCT-1998	98US-0103715P.
PPR	08-OCT-1998	98US-0103717P.
PPR	14-OCT-1998	98US-0104257P.
PPR	20-OCT-1998	98US-0104987P.
PPR	20-OCT-1998	98US-0105000P.
PPR	20-OCT-1998	98US-0105024P.
PPR	21-OCT-1998	98US-0105104P.
PPR	22-OCT-1998	98US-0105169P.
PPR	22-OCT-1998	98US-0105266P.
PPR	26-OCT-1998	98US-0105632P.
PPR	26-OCT-1998	98US-0105634P.
PPR	27-OCT-1998	98US-0105807P.
PPR	27-OCT-1998	98US-0105811P.
PPR	27-OCT-1998	98US-0105812P.
PPR	27-OCT-1998	98US-0106024P.
PPR	28-OCT-1998	98US-0106023P.
PPR	28-OCT-1998	98US-0106029P.
PPR	28-OCT-1998	98US-0106030P.
PPR	28-OCT-1998	98US-0106031P.
PPR	28-OCT-1998	98US-0106178P.
PPR	29-OCT-1998	98US-0106248P.
PPR	29-OCT-1998	98US-0106344P.
PPR	29-OCT-1998	98US-0106350P.
PPR	29-OCT-1998	98US-0106352P.
PPR	30-OCT-1998	98US-0106464P.
PPR	03-NOV-1998	98US-0106856P.
PPR	03-NOV-1998	98US-0106902P.
PPR	03-NOV-1998	98US-0106919P.
PPR	03-NOV-1998	98US-0106942P.
PPR	03-NOV-1998	98US-0106944P.
PPR	10-NOV-1998	98US-0107783P.
PPR	17-NOV-1998	98US-0108775P.
PPR	17-NOV-1998	98US-0108779P.
PPR	17-NOV-1998	98US-0108787P.
PPR	17-NOV-1998	98US-0108789P.
PPR	17-NOV-1998	98US-0108802P.
PPR	17-NOV-1998	98US-0108806P.
PPR	17-NOV-1998	98US-0108807P.
PPR	18-NOV-1998	98US-0108831P.
PPR	18-NOV-1998	98US-0108852P.
PPR	18-NOV-1998	98US-0108853P.
PPR	18-NOV-1998	98US-0108848P.
PPR	18-NOV-1998	98US-0108849P.
PPR	18-NOV-1998	98US-0108850P.
PPR	05-JAN-1999	99W0-US000106.
PPR	16-APR-1999	99US-0129574P.
PPR	23-JULY-1999	99US-0144758P.
PPR	20-JUL-1999	99US-0144758P.

PR	26-JUL-1999;	99US-0145698P.
PR	01-SEP-1999;	99WO-US02011194.
PR	15-SEP-1999;	99WO-US021194.
PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99WO-US023313.
PR	02-DEC-1999;	99WO-US02551.
PR	16-DEC-1999;	99WO-US030095.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US000365.
PR	18-FEB-2000;	2000WO-US000342.
PR	24-FEB-2000;	2000WO-US000304.
PR	02-MAR-2000;	2000WO-US0003841.
PR	15-MAR-2000;	2000WO-US006884.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-JUN-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	23-AUG-2000;	2000WO-US025252.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000WO-US030952.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032678.
PR	28-FEB-2001;	2001WO-US005520.
PR	01-MAR-2001;	2001WO-US006666.
PR	01-JUN-2001;	2001WO-US017800.
PR	01-JUN-2001;	2001WO-US019692.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	04-SEP-2001;	2001US-00946374.
XX		(GETH) GENENTECH INC.
XX		
P1	Baker KP,	Bottstein D,
P1	Gao W,	Desnoy A,
P1	Goddard A,	Godowski E,
P1	Pan J,	Huang M,
P1	Paoi NP,	Ho MR,
P1	Williams FM,	Shi M,
XX	Williams PM,	Wood WI,
WPI:	2003-492259/46	
N-PSDB:	DR-ACH04480.	
PT	Novel secreted and transmembrane protein	
PT	encoding them useful for treating	
PT	disorders, bone and/or cartilage	
PT	arthritis.	
Query	1 MGLS1PLLCLUGLGSQATAP	100.0%;
Best Local Similarity	100.0%	
Matches	248;	Conservative 0;
Qy	1 MGLS1PLLCLUGLGSQATAP	
Db	1 MGLS1PLLCLUGLGSQATAP	
Qy	61 AHCGSGRYWRLGERSLSQL	
Db	61 AHCGSGRYWRLGERSLSQL	
Qy	121 TSSVOPLPLPDCAATGTC	
Db	121 TSSVOPLPLPDCAATGTC	
Qy	181 TSNMYCAGGYGQDAGQGDSC	
Db	181 TSNMYCAGGYGQDAGQGDSC	
Qy	241 IRMINN 248	
Db	241 IRMINN 248	
RESULT	9	
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ID	ABO33512	standard; protein; 248 AA.		98US-0102307P.
XX	AC	ABO33512;	PR	29-SEP-1998;
XX	XX		PR	29-SEP-1998;
DT	17-SEP-2003	(first entry)	PR	29-SEP-1998;
XX	XX	Novel human secreted and transmembrane protein PRO1303.	PR	30-SEP-1998;
DB	XX	Human; secreted and transmembrane protein; PRO; gene therapy; vaccine; tissue typing; chromosome identification; vaccine.	PR	30-SEP-1998;
XX	KW		PR	30-SEP-1998;
XX	KW		PR	01-OCT-1998;
OS	XX		PR	01-OCT-1998;
PN	US2003073129-A1.		PR	01-OCT-1998;
XX	XX		PR	01-OCT-1998;
PD	17-APR-2003.		PR	01-OCT-1998;
XX	XX		PR	01-OCT-1998;
PF	04-SEP-2001:	2001US-00946374.	PR	01-OCT-1998;
XX	XX		PR	01-OCT-1998;
PR	01-SEP-1998;	98US-0098716P.	PR	01-OCT-1998;
PR	01-SEP-1998;	98US-0098723P.	PR	01-OCT-1998;
PR	01-SEP-1998;	98US-0098749P.	PR	01-OCT-1998;
PR	01-SEP-1998;	98US-0098750P.	PR	01-OCT-1998;
PR	02-SEP-1998;	98US-0098803P.	PR	01-OCT-1998;
PR	02-SEP-1998;	98US-0098821P.	PR	01-OCT-1998;
PR	02-SEP-1998;	98US-0098843P.	PR	01-OCT-1998;
PR	09-SEP-1998;	98US-00989536P.	PR	01-OCT-1998;
PR	09-SEP-1998;	98US-0099596P.	PR	01-OCT-1998;
PR	09-SEP-1998;	98US-0099598P.	PR	01-OCT-1998;
PR	09-SEP-1998;	98US-0099602P.	PR	01-OCT-1998;
PR	09-SEP-1998;	98US-0099642P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099741P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099754P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099763P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099792P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099808P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099812P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099815P.	PR	01-OCT-1998;
PR	10-SEP-1998;	98US-0099816P.	PR	01-OCT-1998;
PR	15-SEP-1998;	98US-0100385P.	PR	01-OCT-1998;
PR	15-SEP-1998;	98US-0100388P.	PR	01-OCT-1998;
PR	15-SEP-1998;	98US-0100390P.	PR	01-OCT-1998;
PR	16-SEP-1998;	98US-0100584P.	PR	01-OCT-1998;
PR	16-SEP-1998;	98US-0100627P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-0100661P.	PR	01-OCT-1998;
PR	16-SEP-1998;	98US-0100662P.	PR	01-OCT-1998;
PR	16-SEP-1998;	98US-0100664P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-0100683P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-0100848P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-0100849P.	PR	01-OCT-1998;
PR	18-SEP-1998;	98US-0101014P.	PR	01-OCT-1998;
PR	18-SEP-1998;	98US-0101068P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-0101071P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-01010919P.	PR	01-OCT-1998;
PR	17-SEP-1998;	98US-01011279P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101471P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101472P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101474P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101475P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101476P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101477P.	PR	01-OCT-1998;
PR	23-SEP-1998;	98US-0101479P.	PR	01-OCT-1998;
PR	24-SEP-1998;	98US-0101738P.	PR	01-OCT-1998;
PR	24-SEP-1998;	98US-0101741P.	PR	01-OCT-1998;
PR	24-SEP-1998;	98US-0101743P.	PR	01-OCT-1998;
PR	24-SEP-1998;	98US-0101915P.	PR	01-OCT-1998;
PR	24-SEP-1998;	98US-0101916P.	PR	01-OCT-1998;
PR	29-SEP-1998;	98US-0102207P.	PR	01-OCT-1998;
PR	29-SEP-1998;	98US-0102240P.	PR	01-OCT-1998;
			PR	05-JAN-1999;

PR	12-APR-1999;	99US-00284291.	Db	181 TSNMVCAGGVPGQDQACQGDSGGPLVYCGGLVSGWSVGPCGQDGIPGVTTIICRYVDW 240
PR	16-APR-1999;	99US-0129674P.	Qy	241 IRMIRNN 248
PR	23-JUN-1999;	99US-0141437P.		
PR	20	99US-0144758P.	Db	241 IRMIRNN 248
PR	26-JUL-1999;	99US-0145698P.		
PR	01-SEP-1999;	99WO-US02011.		
PR	15-SEP-1999;	99WO-US02119.		
PR	18-OCT-1999;	99US-00403297.		
PR	30-NOV-1999;	99WO-US028313.		
PR	02-DEC-1999;	99WO-US028551.		
PR	16-DEC-1999;	99WO-US030095.		
PR	05-JAN-2000;	2000WO-US000219.		
PR	06-JAN-2000;	2000WO-US000376.		
PR	11-FEB-2000;	2000WO-US003556.		
PR	18-FEB-2000;	2000WO-US00424.		
PR	24-FEB-2000;	2000WO-US00504.		
PR	02-MAR-2000;	2000WO-US005841.		
PR	15-MAR-2000;	2000WO-US006884.		
PR	17-MAY-2000;	2000WO-US013705.		
PR	22-MAY-2000;	2000WO-US014042.		
PR	30-MAY-2000;	2000WO-US01941.		
PR	01-JUN-2000;	2000WO-US015264.		
PR	23-AUG-2000;	2000WO-US023522.		
PR	24-AUG-2000;	2000WO-US2338.		
PR	08-NOV-2000;	2000WO-US030952.		
PR	10-NOV-2000;	2000WO-US030873.		
PR	01-DEC-2000;	2000WO-US01942.		
PR	28-FEB-2001;	2001WO-US006520.		
PR	01-MAR-2001;	2001WO-US006666.		
PR	01-JUN-2001;	2001US-097205.		
PR	14-JUN-2001;	2001WO-US017801.		
PR	20-JUN-2001;	2001US-00882633.		
PR	29-JUN-2001;	2001WO-US019692.		
PR	09-JUL-2001;	2001WO-US021066.		
XX	XX	XX		
PA	(GETH) GENTENTECH INC.			
PI	Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Pong S;		PR	01-SEP-1998; 98US-0098716P.
PI	Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillian KJ;		PR	01-SEP-1998; 98US-009723P.
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;		PR	01-SEP-1998; 98US-009749P.
PI	Williams PM, Wood WI;		PR	01-SEP-1998; 98US-009750P.
DR	WPI: 2003-585297/55.		PR	02-SEP-1998; 98US-009803P.
XX	XX	XX	PR	02-SEP-1998; 98US-009821P.
PA	N-PSDB; ACD68024.		PR	02-SEP-1998; 98US-009843P.
XX	XX	XX	PR	09-SEP-1998; 98US-009536P.
XX	XX	XX	PR	09-SEP-1998; 98US-009596P.
XX	XX	XX	PR	09-SEP-1998; 98US-009598P.
XX	XX	XX	PR	09-SEP-1998; 98US-009602P.
PT	Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide, and as therapeutic agents e.g. vaccines.		PR	09-SEP-1998; 98US-009642P.
PT	The invention describes an isolated PRO (secreted and transmembrane) polypeptide (1), having at least 80% sequence identity to a sequence		PR	10-SEP-1998; 98US-009741P.
CC	Best Local Similarity 100.0%; Pred. No. 8. 4e-182; Length 248; Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PR	10-SEP-1998; 98US-009816P.
CC	1 MELSIPLVLCLGLSQAATPKLFLNGTEGRNSQPKQVGLPESTSRLRGCVLIDHRVLT 60		PR	15-SEP-1998; 98US-010395P.
CC	1 MELSIPLVLCLGLSQAATPKLFLNGTEGRNSQPKQVGLPESTSRLRGCVLIDHRVLT 60		PR	15-SEP-1998; 98US-010488P.
Qy	61 AHCGSGSNWVRGEHSQSOLNTEQRISGSYTHQIGASTSHEDILRLRLRPLRV 120		PR	15-SEP-1998; 98US-010390P.
Db	61 AHCGSGSNWVRGEHSQSOLNTEQRISGSYTHQIGASTSHEDILRLRLRPLRV 120		PR	16-SEP-1998; 98US-010683P.
Qy	61 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	16-SEP-1998; 98US-010684P.
Db	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	17-SEP-1998; 98US-010684P.
Qy	181 TSNMVCAGGVPGQDADCGSDGGPLVYCGGLVSGWSVGPCGQDGIPGVTTIICRYVDW 240		PR	18-SEP-1998; 98US-0101014P.
Db	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	18-SEP-1998; 98US-0101068P.
Qy	181 TSNMVCAGGVPGQDADCGSDGGPLVYCGGLVSGWSVGPCGQDGIPGVTTIICRYVDW 240		PR	18-SEP-1998; 98US-0101071P.
Db	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	18-SEP-1998; 98US-010930P.
Qy	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	18-SEP-1998; 98US-010948P.
Db	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	19-SEP-1998; 98US-010949P.
Qy	181 TSNMVCAGGVPGQDADCGSDGGPLVYCGGLVSGWSVGPCGQDGIPGVTTIICRYVDW 240		PR	23-SEP-1998; 98US-0101472P.
Db	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	23-SEP-1998; 98US-0101474P.
Qy	181 TSNMVCAGGVPGQDADCGSDGGPLVYCGGLVSGWSVGPCGQDGIPGVTTIICRYVDW 240		PR	23-SEP-1998; 98US-0101475P.
Db	121 TSVQPLPLPNDCATAGTECHYSGKGITNHPRNPFPDLQCLNLTSVHATCHGVPGRI 180		PR	23-SEP-1998; 98US-0101476P.

PR	10-NOV-1998;	98US-0107783D.	Query Match 100.0% ; Score 248; DB 7; Length 248;
PR	17-NOV-1998;	98US-0108775P.	Best Local Similarity 100.0% ; Pred. No. 8 4e-162;
PR	17-NOV-1998;	98US-0108779P.	Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	17-NOV-1998;	98US-0108787P.	
PR	17-NOV-1998;	98US-0108788P.	Qy 1 MGJISIPLLICVLGLSQAATPKIPIFGNTECGRNSQFWQVGLFEGTSLRCGGVFLIDERWVLT A 60
PR	17-NOV-1998;	98US-0108801P.	Db 1 MGJISIPLLICVLGLSQAATPKIPIFGNTECGRNSQFWQVGLFEGTSLRCGGVFLIDERWVLT A 60
PR	17-NOV-1998;	98US-0108802P.	
PR	17-NOV-1998;	98US-0108806P.	
PR	17-NOV-1998;	98US-0108807P.	Qy 61 AHCSGSRTWVLGEHSLQOLDWTEQIIRHSGSPSITHPGYLGASTSHEDIRLLRLRPLPVRY 120
PR	17-NOV-1998;	98US-0108867P.	Db 61 AHCSGSRTWVLGEHSLQOLDWTEQIIRHSGSPSITHPGYLGASTSHEDIRLLRLRPLPVRY 120
PR	17-NOV-1998;	98US-0108925P.	
PR	18-NOV-1998;	98US-0108948P.	Qy 121 TSSVQPLPLPNDCATAGTECHYSGWGTTNHPRAPPDLQLQCLNISIVSHATCHGVPGR 180
PR	18-NOV-1998;	98US-0108849P.	Db 121 TSSVQPLPLPNDCATAGTECHYSGWGTTNHPRAPPDLQLQCLNISIVSHATCHGVPGR 180
PR	18-NOV-1998;	98US-0108850P.	
PR	18-NOV-1998;	98US-0108851P.	
PR	18-NOV-1998;	98US-0108852P.	
PR	18-NOV-1998;	98US-0108858P.	Qy 181 TSANAVCAGSVPGODAACQDSGGPLVVCGLVQGLVWSWGSYVGPCGODGIPGVYTYICKYDW 240
PR	18-NOV-1998;	98US-0108904P.	Db 181 TSANAVCAGSVPGODAACQDSGGPLVVCGLVQGLVWSWGSYVGPCGODGIPGVYTYICKYDW 240
PR	22-DEC-1998;	98US-0113296P.	
PR	30-DEC-1998;	98US-0114223P.	
PR	05-JAN-1999;	99WO-US0000106.	Qy 241 IRMTMRNN 248
PR	16-APR-1999;	99US-0129674P.	Db 241 IRMTMRNN 248
PR	23-JUN-1999;	99US-0141037P.	
PR	20-JUL-1999;	99US-0144758P.	
PR	26-JUL-1999;	99US-0145698P.	
PR	01-SBP-1999;	99US-0114223P.	
PR	15-SBP-1999;	99WO-US020111.	
PR	29-OCT-1999;	99US-0162506P.	RESULT 12 ADD39786 standard; protein: 248 AA.
PR	30-NOV-1999;	99WO-US028313.	XX
PR	02-DEC-1999;	99WO-US028551.	AC
PR	16-DEC-1999;	99WO-US030095.	XX
PR	05-JAN-2000;	20000KO-US000219.	DT 15-JAN-2004 (first entry)
PR	06-JAN-2000;	20000KO-US000376.	XX
PR	11-FEB-2000;	20000KO-US003565.	DB Human secreted/transmembrane protein PRO1203.
PR	18-FEB-2000;	20000KO-US00434.	XX
PR	24-FEB-2000;	20000KO-US005004.	KW Human; secreted protein; transmembrane protein; PRO; tumour;
PR	02-MAR-2000;	20000KO-US010584.	KW immune response; cardiac insufficiency disorder; calcium flux;
PR	15-MAR-2000;	20000KO-US006884.	KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
PR	17-MAY-2000;	20000KO-US013705.	KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
PR	30-MAY-2000;	20000KO-US1104.	KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
PR	02-JUN-2000;	20000KO-US014941.	KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
PR	23-AUG-2000;	20000KO-US0215264.	XX
PR	24-AUG-2000;	20000KO-US023328.	OS Homo sapiens.
PR	08-NOV-2000;	20000KO-US030952.	XX
PR	10-NOV-2000;	20000KO-US030873.	PN US2003033462-A1.
PR	01-DEC-2000;	20000KO-US032678.	XX
PR	28-FEB-2001;	20010W-US006520.	PD 01-MAY-2003.
PR	01-MAR-2001;	20010W-US006660.	XX
PR	01-JUN-2001;	20010W-US017800.	10-DBC-2001; 20010US-00013913.
PR	20-JUN-2001;	20010W-US019692.	XX
PR	29-JUN-2001;	20010W-US021062.	PR 05-JAN-1999; 99WO-US000106.
PR	09-JUL-2001;	20010W-US021755.	PR 01-SEP-1999; 99WO-US020111.
PR	04-SEP-2001;	20010W-US0946374.	PR 15-SEP-1999; 99WO-US021194.
XX			PR 30-NOV-1999; 99WO-US028313.
PA (GETH) GENENTECH INC.			PR 02-DEC-1999; 99WO-US028551.
XX			PR 16-DEC-1999; 99WO-US030095.
PR			PR 05-JAN-2000; 20000KO-US000219.
PR			PR 06-JAN-2000; 20000KO-US00376.
PR			PR 11-FEB-2000; 20000KO-US03565.
PR			PR 18-FEB-2000; 20000KO-US014941.
PR			PR 02-JUN-2000; 20000KO-US014342.
PR			PR 23-AUG-2000; 20000KO-US015004.
PR			PR 02-MAR-2000; 20000KO-US015841.
PR			PR 15-MAR-2000; 20000KO-US006884.
PR			PR 17-MAY-2000; 20000KO-US013705.
PR			PR 22-MAY-2000; 20000KO-US014042.
PR			PR 30-MAY-2000; 20000KO-US014941.
PR			PR 02-JUN-2000; 20000KO-US015264.
PR			PR 23-AUG-2000; 20000KO-US123522.
PR			PR 24-AUG-2000; 20000KO-US023328.
PR			PR 08-NOV-2000; 20000KO-US009052.
PR			PR 10-NOV-2000; 20000KO-US030873.
PR			PR 01-DEC-2000; 20000KO-US032678.
PR			PR 04-SEP-2001; 20010W-US0946374.
XX			XX
PI	Baker KP, Bottstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Hillian JW, Gao W, Goddard A, Grimaldi JC, Gurney AU, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tomas D, Watanabe CK, Williams PM, Wood WI;		The invention relates to an isolated PRO polypeptide (secreted or
XX			Claim 12; SEQ ID NO 194; 55pp; English.
XX			CC

PR 01-MAR-2001; 2001IW0-US006666.	Db 181 TSNMTCAGGTPQDAGQDSSGGPLVCGVTLQGLVSMGSVGPQDGSIPIGVYTYICKVWD 240
PR 01-JUN-2001; 2001IW0-US01780.	
PR 20-JUN-2001; 2001IW0-US019692.	
PR 29-JUN-2001; 2001IW0-US021066.	
PR 09-JUL-2001; 2001IW0-US021735.	
PR 04-SEP-2001; 2001US-00946374.	
XX PA) GENENTECH INC.	
XX DR ; ADD39785.	
PT Baker KP, Bostein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;	
PI Gao W, Goddard A, Godowski BJ, Grimaldi JC, Gurney AL, Hillian KJ,	
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas P, Watanabe CK;	
PI Williams PM, Wood WI;	
XX WPI ; 2003-755122/71.	
XX DR ; ADD70232;	
PT New secreted and transmembrane PRO polypeptides useful for treating	
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or	
PT hypo-insulinemia, sports injuries and arthritis.	
XX PS Claim 12; SEQ ID NO 194; 557P; English.	
CC The invention relates to an isolated PRO polypeptide (secreted or	
CC transmembrane protein) having at least 80% amino acid sequence identity	
CC to an amino acid sequence chosen from 123 fully defined sequences as	
CC given in the specification (including their extracellular domains either	
CC or without their associated signal peptides. Also include are the	
CC nucleotide (NA) sequences encoding PRO, a vector comprising PRO, a chimaeric molecule	
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-	
CC PRO antibody. PRO is useful as molecular weight markers for protein	
CC electrophoresis and also for chromosome identification. PRO is also	
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation	
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is	
CC useful for generating transgenic animals or knock-out animals which are	
CC useful in development and screening useful reagents. PRO NA is also	
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are	
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410	
CC polypeptides are useful for suppressing immune response. PRO1246	
CC polypeptide is useful for treating cardiac insufficiency disorders.	
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and	
CC PRO1561 polypeptide are useful for stimulating calcium flux in human	
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474	
CC polypeptides are useful for treating bone and/or cartilage disorders	
CC (e.g., arthritis) and wound healing. PRO130, PRO1275 and PRO1418	
CC polypeptides are useful for treating diabetes in skeletal muscle cells	
CC and obesity. PRO1265, PRO1244 and PRO138 polypeptides are useful for	
CC treating Berger disease or other nephropathies associated with Schonlein-	
CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's	
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO118,	
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present	
CC sequence represents a PRO protein of the invention.	
XX SQ Sequence 248 AA;	
Query Match 100.0%; Score 248; DB 7; Length 248;	
Best Local Similarity 100.0%; Pred. No. 8.4e-182;	
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 MGLSIPPLCIVGLSQAATPKIFNGTBCGRNSQPQVQGLFEGTSURCGVGLIDIRWVLTAA 60	
Db 1 MGLSIPPLCIVGLSQAATPKIFNGTBCGRNSQPQVQGLFEGTSURCGVGLIDIRWVLTAA 60	
Qy 61 AHCGSGSRVYVRLGEHSLQDWTQEIRHSGFSYTHPGLGASTSHBHDLLRLRLPVRV 120	
Db 61 AHCGSGSRVYVRLGEHSLQDWTQEIRHSGFSYTHPGLGASTSHBHDLLRLRLPVRV 120	
Qy 121 TSSVQPLPLNDCATGTECHVSGCITIHEPRNPFDLQCLNLIVSHATCHGVPGR 180	
Db 121 TSSVQPLPLNDCATGTECHVSGCITIHEPRNPFDLQCLNLIVSHATCHGVPGR 180	
Qy 181 TSNNYCAGGYPGQDAGQDSSGGPLVCGVTLQGLVSMGSVGPQDGSIPIGVYTYICKVWD 240	

PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101474P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 01-OCT-1998; 98US-0102484P.
 PR 02-OCT-1998; 98US-0102485P.
 PR 06-OCT-1998; 98US-0102487P.
 PR 30-OCT-1998; 98US-0102570P.
 PR 07-OCT-1998; 98US-0102571P.
 PR 07-OCT-1998; 98US-0102684P.
 PR 07-OCT-1998; 98US-0102687P.
 PR 07-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 07-OCT-1998; 98US-0103449P.
 PR 08-OCT-1998; 98US-0103314P.
 PR 08-OCT-1998; 98US-0103315P.
 PR 08-OCT-1998; 98US-010328P.
 PR 08-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 20-OCT-1998; 98US-0103401P.
 PR 20-OCT-1998; 98US-0103433P.
 PR 20-OCT-1998; 98US-0103678P.
 PR 21-OCT-1998; 98US-0103679P.
 PR 22-OCT-1998; 98US-010371P.
 PR 22-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-010500P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 27-OCT-1998; 98US-0105104P.
 PR 28-OCT-1998; 98US-0105169P.
 PR 28-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105594P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105811P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 28-OCT-1998; 98US-0106023P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106171P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106310P.
 PR 29-OCT-1998; 98US-0106344P.
 PR 03-NOV-1998; 98US-0106319P.
 PR 03-NOV-1998; 98US-0106324P.
 PR 03-NOV-1998; 98US-0106464P.
 PR 03-NOV-1998; 98US-0106856P.
 PR 03-NOV-1998; 98US-0106902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.

PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108948P.
 PR 18-NOV-1998; 98US-0108949P.
 PR 18-NOV-1998; 98US-0108950P.
 PR 18-NOV-1998; 98US-0108951P.
 PR 18-NOV-1998; 98US-0108952P.
 PR 18-NOV-1998; 98US-0108958P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99WO-US021194.
 PR 23-JUN-1999; 99WO-US129674P.
 PR 30-NOV-1999; 99WO-US023313.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US000376.
 PR 29-OCT-1999; 99US-0162506P.
 PR 23-JUN-1999; 99US-0144037P.
 PR 02-DEC-1999; 99WO-US025551.
 PR 02-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US0013565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 05-MAR-2000; 2000WO-US002119.
 PR 06-MAR-2000; 2000WO-US000376.
 PR 11-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 28-MAY-2000; 2000WO-US014941.
 PR 30-MAY-2000; 2000WO-US02678.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US03522.
 PR 24-AUG-2000; 2000WO-US03328.
 PR 08-NOV-2000; 2000WO-US00952.
 PR 10-NOV-2000; 2000WO-US00873.
 PR 01-DEC-2000; 2000WO-US021735.
 PR 04-SEP-2001; 2001WO-US00946374.
 XX (GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Baton DL, Ferrara N, Fong S, Gurney AL, Grimaldi JC, Hillan KJ, Goddard A, Godowski PJ, Pan J, Paoni NF, Smith V, Stewart RA, Williams PM, Wood WI, Watanabe CK;

PI PR 01-JUN-2001; 2001WO-US017800.
 PI PR 20-JUN-2001; 2001WO-US019692.
 PI PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 DR WPI ; 2003-70844/67.
 DR N-PSPDB; ADD70331.

CC The invention relates to an isolated PRO polypeptide (secreted or modulating tissue typing, modulating molecular weight markers in protein electrophoresis, for treating arthritis, tumor.

PT Novel isolated PRO polypeptide useful for tissue typing, modulating biological activity of cell, as molecular weight markers in protein electrophoresis, for treating arthritis, tumor.

Best Local Similarity 100.0%; Score 248; DB 7; Length 248;
 Matches 248; Conservative 0; Mismatches 0; Gaps 0;

Query 1 MGLSFLLCVGQAAATPKIFNGTBCGANSQPVQVGLPECTSLRGCGTLIDHRYVLTAA 60
 Database 1 MGLSFLLCVGQAAATPKIFNGTBCGANSQPVQVGLPECTSLRGCGVLIDHRYVLTAA 60

Qy	61	AHCSGSRVWRLGBHSISOLDWTEQIRHSGFSTHPCYLGASTSHEDLRLRLPVRV	120	PR	17-SEP-1998;	98US-0100711P.
Db	61	AHCSGSRVWRLGBHSISOLDWTEQIRHSGFSTHPCYLGASTSHEDLRLRLPVRV	120	PR	17-SEP-1998;	98US-0100919P.
Db	121	TSSVQPLPLNDCATAGTECHYSGMGTINHPRNPFPDLLQCLNLSTVSHATCHGIVYGPRI	180	PR	18-SEP-1998;	98US-0100848P.
Qy	121	TSSVQPLPLNDCATAGTECHYSGMGTINHPRNPFPDLLQCLNLSTVSHATCHGIVYGPRI	180	PR	18-SEP-1998;	98US-0100849P.
Db	181	TSMVCAAGGVPQDADCGQDSSGSLVCCVLQGIVSVESVGPGQDG1PGVYTYICKYDW	240	PR	18-SEP-1998;	98US-0101044P.
Qy	181	TSMVCAAGGVPQDADCGQDSSGSLVCCVLQGIVSVESVGPGQDG1PGVYTYICKYDW	240	PR	18-SEP-1998;	98US-0101045P.
Db	241	IRMIMRHN 248		PR	22-SEP-1998;	98US-0101219P.
Qy	241	IRMIMRHN 248		PR	23-SEP-1998;	98US-0101471P.
Db	241	IRMIMRHN 248		PR	23-SEP-1998;	98US-0101472P.
Qy				PR	23-SEP-1998;	98US-0101474P.
Db				PR	23-SEP-1998;	98US-0101475P.
Qy				PR	23-SEP-1998;	98US-0101476P.
Db				PR	23-SEP-1998;	98US-0101477P.
RESLT 14				PR	23-SEP-1998;	98US-0101479P.
ADD38353				PR	24-SEP-1998;	98US-010138P.
ID ADD38353		standard; protein; 248 AA.		PR	24-SEP-1998;	98US-0101945P.
XX				PR	24-SEP-1998;	98US-0101916P.
AC ADD38353;				PR	29-SEP-1998;	98US-0102207P.
AC				PR	29-SEP-1998;	98US-0102240P.
XX				PR	29-SEP-1998;	98US-0102307P.
DT 15-JAN-2004		(first entry)		PR	29-SEP-1998;	98US-0102330P.
XX				PR	29-SEP-1998;	98US-0102331P.
DE Human secreted/transmembrane protein PRO1303.				PR	30-SEP-1998;	98US-0102484P.
XX				PR	30-SEP-1998;	98US-0102487P.
KW Human; secreted protein; transmembrane protein; PRO; tumour;				PR	30-SEP-1998;	98US-0102570P.
KW immune response; cardiac insufficiency disorder; calcium flux;				PR	30-SEP-1998;	98US-0102571P.
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;				PR	01-OCT-1998;	98US-0102684P.
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;				PR	01-OCT-1998;	98US-0102687P.
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;				PR	02-OCT-1998;	98US-0102655P.
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.				PR	06-OCT-1998;	98US-0103258P.
XX				PR	06-OCT-1998;	98US-0103449P.
OS Homo sapiens.				PR	07-OCT-1998;	98US-0103314P.
XX				PR	07-OCT-1998;	98US-0103315P.
PN US2003096955-A1.				PR	07-OCT-1998;	98US-0103328P.
XX				PR	07-OCT-1998;	98US-0103335P.
PD 22-MAY-2003.				PR	07-OCT-1998;	98US-0103336P.
XX				PR	07-OCT-1998;	98US-0103401P.
PP 07-DBC-2001; 2001US-00012755.				PR	08-OCT-1998;	98US-0103633P.
XX				PR	08-OCT-1998;	98US-0103678P.
PR 01-SEP-1998;	98US-0098716P.			PR	08-OCT-1998;	98US-0103679P.
PR 01-SEP-1998;	98US-0098723P.			PR	08-OCT-1998;	98US-0103711P.
PR 01-SEP-1998;	98US-0098779P.			PR	14-OCT-1998;	98US-0104227P.
PR 02-SEP-1998;	98US-0098750P.			PR	20-OCT-1998;	98US-0105000P.
PR 02-SEP-1998;	98US-0098803P.			PR	20-OCT-1998;	98US-0105002P.
PR 02-SEP-1998;	98US-0098821P.			PR	21-OCT-1998;	98US-0105104P.
PR 09-SEP-1998;	98US-0098843P.			PR	22-OCT-1998;	98US-0105119P.
PR 09-SEP-1998;	98US-0099536P.			PR	27-OCT-1998;	98US-0105266P.
PR 09-SEP-1998;	98US-0099599P.			PR	26-OCT-1998;	98US-010593P.
PR 09-SEP-1998;	98US-0099792P.			PR	26-OCT-1998;	98US-010623P.
PR 09-SEP-1998;	98US-0099602P.			PR	28-OCT-1998;	98US-010624P.
PR 09-SEP-1998;	98US-0099642P.			PR	29-OCT-1998;	98US-010629P.
PR 10-SEP-1998;	98US-0099812P.			PR	28-OCT-1998;	98US-010630P.
PR 10-SEP-1998;	98US-0099815P.			PR	29-OCT-1998;	98US-010632P.
PR 10-SEP-1998;	98US-0099816P.			PR	30-OCT-1998;	98US-010634P.
PR 15-SEP-1998;	98US-0100388P.			PR	28-OCT-1998;	98US-010636P.
PR 15-SEP-1998;	98US-010388P.			PR	28-OCT-1998;	98US-0106384P.
PR 15-SEP-1998;	98US-0100390P.			PR	29-OCT-1998;	98US-01065010P.
PR 16-SEP-1998;	98US-0100564P.			PR	30-OCT-1998;	98US-0106532P.
PR 16-SEP-1998;	98US-010622P.			PR	03-NOV-1998;	98US-0106846P.
PR 16-SEP-1998;	98US-0100661P.			PR	03-NOV-1998;	98US-0106902P.
PR 16-SEP-1998;	98US-0100662P.			PR	03-NOV-1998;	98US-0106905P.
PR 17-SEP-1998;	98US-0100664P.			PR	03-NOV-1998;	98US-0106919P.
PR 17-SEP-1998;	98US-0100663P.			PR	03-NOV-1998;	98US-0106922P.
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Sequence Data							
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PR	16-APR-1999;	99WO-US000106.					
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PR	18-FEB-2000;	2000WO-US004342.					
PR	24-FEB-2000;	2000WO-US005004.					
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PR	15-MAR-2000;	2000WO-US006884.					
PR	17-MAY-2000;	2000WO-US013705.					
PR	22-MAY-2000;	2000WO-US014044.					
PR	30-MAY-2000;	2000WO-US014941.					
PR	02-JUN-2000;	2000WO-US015264.					
PR	23-AUG-2000;	2000WO-US0158P.					
PR	24-AUG-2000;	2000WO-US023522.					
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PA	(GETH) GENENTECH INC.						
PA	Baker KP, Botstein D, Destroyers L, Baton DL, Ferrara N, Fong S;						
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PI	Gao W,	Goddard A,	Grimaldi JC,	Gurney AL,	Hillan KJ;		
PI	Pan J,	Paozi NP,	Roy MA,	Smith V,	Stewart TA,	Watanaabe CK;	
PI	Williams PM,	Wood WI,					
DR	WPI; 2003-787000/74.						
DR	N-PSDB; ADD18352.						
XX	Novel isolated PRO polypeptide, useful for treating cancerous tumors, cardiac insufficiency disorders, wound healing, diabetes mellitus, thalassemias.						
PS	Claim 12; SEQ ID NO 194; 556pp; English.						
XX	The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity						
CC	10-SEP-1998;	98US-010085P.					
CC	15-SEP-1998;	98US-010088P.					

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PR	16-SEP-1998;	98US-0100661P.	PR	30-OCT-1998;	98US-0106464P.
PR	16-SEP-1998;	98US-0100662P.	PR	03-NOV-1998;	98US-0106856P.
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PR	30-SEP-1998;	98US-010249P.	PR	05-JAN-1999;	99W0-US00106.
PR	30-SEP-1998;	98US-0102207P.	PR	16-APR-1999;	99W0-US01194.
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PR	29-SEP-1998;	98US-0102330P.	PR	20-JUL-1999;	99US-014758P.
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PR	06-OCT-1998;	98US-0102487P.	PR	15-SEP-1999;	99W0-US01194.
PR	07-OCT-1998;	98US-0102240P.	PR	29-OCT-1999;	99W0-US01199.
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PR	02-OCT-1998;	98US-0102865P.	PR	05-JAN-2000;	2000W0-US00219.
PR	07-OCT-1998;	98US-0103258P.	PR	06-JAN-2000;	2000W0-US00376.
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PR	07-OCT-1998;	98US-0103314P.	PR	19-FEB-2000;	2000W0-US004342.
PR	07-OCT-1998;	98US-0103315P.	PR	24-FEB-2000;	2000W0-US005004.
PR	08-OCT-1998;	98US-0103328P.	PR	02-MAR-2000;	2000W0-US03522.
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PR	14-OCT-1998;	98US-010457P.	PR	08-NOV-2000;	2000W0-US0052.
PR	20-OCT-1998;	98US-0104387P.	PR	17-MAY-2000;	2000W0-US03705.
PR	26-OCT-1998;	98US-0105000P.	PR	22-MAY-2000;	2000W0-US01042.
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PR	22-OCT-1998;	98US-0105169P.	PR	01-JUN-2001;	2001W0-US03328.
PR	28-OCT-1998;	98US-010563P.	PR	08-NOV-2001;	2000W0-US017800.
PR	28-OCT-1998;	98US-0106030P.	PR	20-JUN-2001;	2001W0-US019692.
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PR	27-OCT-1998;	98US-010581P.	XX	XX	(GETH) GENENTECH INC.
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PR	28-OCT-1998;	98US-0106032P.	PI	PI	Pan J, Paoni NP, Roy NB, Smith V, Stewart RA, Thomas D, Williams PM, Wood WI;
PR	28-OCT-1998;	98US-0106033P.	PI	PI	WPI; 2003-786999/74.

DR N-PSDB; ADD39308.

XX Novel isolated PRO polypeptide useful for tissue typing, modulating
 PT biological activity of cell, as molecular weight markers in protein
 PT electrophoresis, for treating arthritis, tumor.

XX Claim 12: SEQ ID NO 194; 550pp; English.

XX The invention relates to an isolated PRO polypeptide (secreted or

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Qy	181	TSNNVCAGGVPKGODACQEDGGPLVGGTLQGLYSWGSVGPCCODGIPGVVTTICKWDW	240
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Qy	241	IRIMMRNN 248	
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Search completed: June 16, 2004, 15:13:31
 Job time : 61 secs

Copyright (c) 1993 - 2004 Compugen Ltd.	Gendcore version 5.1.6	30	11	4.4	264	2	I38136
OM protein - protein search, using SW model		31	11	4.4	266	2	JC4850
Run on:	June 16, 2004, 15:11:22 ; search time 21 Seconds (without alignments)	32	11	4.4	270	2	S56160
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N;Alternate names: adipsin; C3 convertase activator							
C;Species: Homo sapiens (man)							
C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 08-Dec-2000							
C;Accession: A40197; A00936; S66645							
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S. J. Biol. Chem. 267, 9210-9213, 1992							
A;Title: Human adipsin is identical to complement factor D and is expressed at high lev							
A;Reference number: A40197; MUID:92250520; PMID:1374388							
A;Accession: A40197							
A;Molecule type: mRNA							
A;Residues: 1-246 <WHL>							
A;Cross references: GB:MB4526							
A;Biemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E. Biochemistry 23, 2482-2486, 1984							
A;Title: Amino acid sequence of human D of the alternative complement pathway.							
A;Reference number: A00936; MUID:85000441; PMID:6383466							
A;Accession: A00936							
A;Molecule type: protein							
A;Residues: 19-44; G, '46-51, 'Q, '53-75, 'TH, '78, 'P, '80-83, 'XXXITIE', '90-172, '86-91, '185-235, R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Yamada, Immunol. 27, 637-644, 1990							
A;Title: Molecular and functional identification and purification of complement compone							
A;Reference number: A60571; MUID:90370044; PMID:2395435							
A;Accession: A60571							
A;Molecule type: protein							
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R;Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H. FEBS Lett. 371, 300-302, 1995							
A;Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complemen							
A;Reference number: S66645; MUID:96013156; PMID:7556615							
A;Accession: S66645							
A;Status: preliminary							
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A;Gene: GDB:DF							
A;Cross references: GDB:132645; OMIM:134350							
C;Superfamily: trypsin homology							
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase							
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F;59,105,201/Active site: His, Asp, Ser #statut predicted							
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	13	5.2	431	2	JS0599		t-plasminogen acti
4	13	5.2	477	1	A34369		t-plasminogen acti
5	13	5.2	477	2	JS0597		t-plasminogen acti
6	13	5.2	477	2	JS0598		t-plasminogen acti
7	13	5.2	559	1	A35029		t-plasminogen acti
8	13	5.2	559	1	A29941		t-plasminogen acti
9	13	5.2	562	1	URKHUT		coagulation factor
10	13	5.2	593	2	S45281		coagulation factor
11	13	5.2	603	2	S28941		coagulation factor
12	13	5.2	615	1	KFHU12		polyprotein - Afri
13	13	5.2	1524	2	T30327		compromotor factor
14	12	4.8	191	2	S54115		trypsin-like prote
15	12	4.8	254	2	S65465		trypsin-like prote
16	12	4.8	256	1	TRPF		trypsin-like prote
17	12	4.8	264	2	S32794		trypsin-like prote
18	12	4.8	267	2	S40006		trypsin (EC 3.4.21
19	12	4.8	271	2	S41308		serine proteinase
20	12	4.8	274	2	S35339		trypsin (EC 3.4.21
21	12	4.8	275	2	S40007		trypsin (EC 3.4.21
22	12	4.8	275	2	S40005		trypsin (EC 3.4.21
23	12	4.8	277	2	T35240		probable serine pr
24	12	4.8	285	2	T35195		chymotrypsin-like
25	11	4.4	126	2	A23473		probable serine pr
26	11	4.4	225	2	S55356		serine proteinase
27	11	4.4	237	2	S55378		tryptase (EC 3.4.2
28	11	4.4	237	2	S68702		neurosin - mouse
29	11	4.4	260	2	I565559		

P;2721_321_428/Active site: His, Asp, Ser #status predicted						
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Db	422	DACQGDSGGPLVC	434			
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N;Alternate names: tissue plasminogen activator						
C;Species: Desmodus rotundus (common vampire bat)						
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999						
C;Accession: JS0598						
R;Kraetzschmar, J. ; Haendler, B. ; Langer, G. ; Boidol, W. ; Bringmann, P. ; Alagon, A. ; Don						
Gene 105 , 229-237 , 1991						
A;Title: The Plasminogen activator family from the salivary gland of the vampire bat Des						
A;Reference number: JS0597; MUID:92039036; PMID:1937019						
A;Accession: JS0598						
A;Molecule type: mRNA						
A;Residues: 1-477 <RRA>						
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F;18-209/Domain: kringle homology <KRG>						
F;226-371/Domain: tryptophan homology <TRY>						
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P;185,198/Binding site: carbohydrate (Asn) (covalent) #status predicted						
P;225-226/Cleavage site: H16-Ser (plasmin) #status predicted						
P;272,321,428/Active site: His, Asp, Ser #status predicted						
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Best Local Similarity	100.0%	Pred. No	5.1e-05;			
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C;Species: Rattus norvegicus (Norway rat)						
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999						
C;Accession: A35029; A31597						
R;Feng, P. ; Ohlsson, M. ; NY, T.						
J. Biol. Chem. 265 , 2022-2027 , 1990						
A;Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec						
A;Reference number: A35029; MUID:9013048; PMID:2105315						
A;Accession: A35029						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-559 <PEN>						
A;Cross-references: GB:M31197; NID:gi207429; PIDN:AAA42261.1; PMID:gi207431; GB:J05226						
R;NY, T. ; Leonardsen, G. ; Hsueh, A.J.W.						
DNA 7 , 671-677 , 1988						
A;Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activator						
A;Reference number: A31597; MUID:89170114; PMID:3148445						
A;Accession: A31597						
A;Status: preliminary						
A;Molecule type: mRNA						
A;Residues: 1-379 , 'K' , 381-559 <NTT>						
A;Cross-references: GB:M31059; NID:gi30159; PIDN:AAA41812.1; PMID:gi50160						
C;Superfamily: tissue plasminogen activator; EGP homology; fibronectin type I repeat hom						

Qy 194 DACQDGGPLVC 206
 Db ||||| ||||| |||||
 504 DACQDGGPLVC 516

RESULT 9

URERU t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human
 N;Alternate names: t-PA; tissue plasminogen activator

C;Species: Homo sapiens (man)

C;Accession: A94004; #sequence revision 14-Nov-1983 #text change 08-Dec-2000

R;Ny, T.; Eligh, F.; Lund, B.

Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984

A;Title: The structure of the human tissue-type plasminogen activator gene: correlation

A;Accession number: A94004; MUID:84298137; PMID:6089198

A;Molecule type: DNA

A;Cross-references: GB:K03021; PIDN:AAA98809_1; PID:g339818

R;Itagaki, Y.; Yusa, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.

Agric. Biol. Chem. 55, 1225-1232, 1991

A;Title: The human tissue plasminogen activator gene

A;Accession number: A23529; MUID:86196143; PMID:3009482

A;Molecule type: DNA

A;Residues: 1-562 <DB>

A;Cross-references: PIDN:9339817; PIDN:AAA98809_1; PID:g339818

R;Pennica, D.; Holmes, W.E.; Kohr, W.J.; Hardwick, R.N.; Vehar, G.A.; Bennett, C.A.; Bennett, NATURE 301, 214-221, 1983

A;Title: Purification and characterization of tissue plasminogen activator secreted by

A;Reference number: J00562; MUID:91291340; PMID:1368831

A;Accession: J00562

A;Molecule type: mRNA

A;Residues: 31-562 <ITAA>

A;Cross-references: DDBJ:01096; PIDN:g220128; PIDN:BA00081_1; PID:g441174

A;Experimental source: embryonic lung fibroblast IMR-90 cells

A;Note: Part of this sequence, including the amino end of the mature protein, was confirmed

R;Pennica, D.; Holmes, W.E.; Kohr, W.J.; Hardwick, R.N.; Vehar, G.A.; Ward, C.A.; Bennett,

Nucleic Acids Res. 16, 5695, 1988

A;Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe

A;Accession number: S02125; MUID:88262579; PMID:313340

A;Accession: A93293

A;Molecule type: mRNA

A;Residues: 1-562 <PEN>

A;Cross-references: GB:L00141

A;Experimental source: melanoma Cells

R;Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.

FETAL LUNG CELLS ATCC-138

Nucleic Acids Res. 16, 5695, 1988

A;Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche

A;Accession number: A93293; MUID:83115262; PMID:6337343

A;Status: translation not shown

A;Accession: A91343; MUID:3896853

A;Molecule type: mRNA

A;Residues: 1-562 <SAS>

A;Cross-references: EMBL:X07393; PID:937243; PID:CAA30302_1; PID:937244

A;Experimental source: fetal lung cells

R;Ragitani, H.; Tagawa, M.; Hatangaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma-

FFBS Lett. 189, 145-149, 1985

A;Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen

A;Reference number: A91343; MUID:852285620; PMID:3896853

A;Molecule type: mRNA

A;Residues: 1-38, 'G', 86-433, 'B', 435-562 <RG>

A;Cross-references: Detroit 562 cells; ATCC-138

R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, S.; Josephson, S.

Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983

A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ

A;Reference number: A93951; MUID:8316956; PMID:6572297

A;Accession: A93951

A;Molecule type: mRNA

A;Residues: 251-358 <EDL>

A;Experimental source: melanoma cells
 R;Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
 Biochemistry 23, 3701-3707, 1984

A;Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived a differences.

A;Reference number: A90488; MUID:85000468; PMID:6433976

A;Contents: annotation: melanoma cells; partial sequence of residues 36-562, active and
 R;Pohl, G.; Kaplan, L.; Binarragon, M.; Wallen, P.; Jornvall, H.
 FEBS Lett. 168, 29-32, 1984

A;Title: Differences between uterine and melanoma forms of tissue plasminogen activator

A;Reference number: A91322; MUID:84158956; PMID:6538514

A;Experimental source: uterus

A;Residues: 33-45;31-320 <POH>

A;Molecule type: protein

A;Accession: A91322

A;Note: In the uterus, cleavage of the activation peptide may also occur after 38-Gln

R;van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
 J. Biol. Chem. 261, 14214-14218, 1986

A;Contents: annotation: fibrin binding site

A;Reference number: A37567; MUID:87033611; PMID:3021732

A;Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen a

A;Reference number: A37568; MUID:89161761; PMID:3030730

A;Contents: annotation: fibrin binding site

R;Dodd, I.; Nunn, B.; Robinson, J. H.
 Thromb. Haemost. 59, 523-528, 1988

A;Title: Isolation, identification and pharmacokinetic properties of human tissue-type

A;Reference number: A60902; MUID:89044681; PMID:3142086

A;Contents: annotation: novel forms of expressed recombinant t-PA

R;Harris, T.J.R.; Patel, T.; Marton, F.A.O.; Little, S.; Bmtage, J.S.; Opdenakker, G.;
 Mol. Biol. Med. 3, 279-292, 1986

A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its exp

A;Accession number: 16010; MUID:3090401

A;Accession: A54645; MUID:86284200; PMID:3090401

A;Molecule type: mRNA

A;Residues: 1-562 <HR>

A;Cross-references: GB:MM15518; PID:g190031; PIDN:AAA60111_1; PID:9190032

A;Contents: annotation: parts of this sequence were confirmed by peptide sequencing

A;Note: Parts of this sequence were confirmed by peptide sequencing

R;Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
 J. Biol. Chem. 260, 11223-11230, 1985

A;Title: Expression of human uterine tissue-type plasminogen activator in mouse cells u

A;Reference number: 155232; MUID:8528338; PMID:3161893

A;Accession: 16010

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-562 <RES>

A;Cross-references: GB:MM18102; PID:g340176; PIDN:AAA6800_1; PID:9340177

R;Fisher, R.; Waller, B.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
 J. Biol. Chem. 261, 461-472, 1987

A;Title: Isolation and characterization of the human tissue-type plasminogen activator

A;Reference number: 155232

A;Accession: 155232

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-36 <REB2>

A;Cross-references: GB:MM1890; PID:9319837; PIDN:AAA61213_1; PID:9339839

C;Comment: Cleavage by Plasmin or trypsin does not hold together by a single

C;Keywords: fibrinolytic activator; EGf homology; fibronectin type I repeat ho

F;1-23/Domain: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. I

C;Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.

C;Genetic:

A;Gene: GDB:PIAT

A;Cross-references: GDB:119496; OMIM:173370

A;Molecule type: mRNA

A;Introns: 2/3; 39/1; 85/1; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 51

A;Supfamily: tissue plasminogen activator; EGf homology; fibronectin type I repeat ho

R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, S.; Josephson, S.
 Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983

A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ

A;Reference number: A93951; MUID:8316956; PMID:6572297

A;Accession: A93951

A;Molecule type: protein

A;Cross-references: GDB:119496; OMIM:173370

A;Molecule type: mRNA

A;Residues: 1-38, 'G', 86-433, 'B', 435-562 <RG>

A;Cross-references: Detroit 562 cells; ATCC-138

R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, S.; Josephson, S.
 Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983

A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ

A;Reference number: A93951; MUID:8316956; PMID:6572297

A;Accession: A93951

A;Molecule type: mRNA

A;Residues: 251-358 <EDL>

A;Cross-references: GDB:119496; OMIM:173370

P;127-208/Domain: kringle homology <TRY>
 P;215-296/Domain: kringle homology <KR2>
 P;311-562/Product: t- β -aminogen activator chain B #status experimental <BCN>
 P;311-556/Domain: trypsin homology <TRY>
 P;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-291,299-4
 P;152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
 P;219/Binding site: carbohydrate (Asn) (covalent) #status experimental
 P;310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental
 P;357,406/Active site: His, Asp #status predicted
 P;513/Active site: Ser #status experimental.

Query Match 5.2%; Score 13; DB 1; Length 562;
 Best Local Similarity 100.0%; Pred. No. 5.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQGDGGPLVC 206
 Db 507 DACQGDGGPLVC 519

RESULT 10

S45281 coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
 N;Alternate names: Hageman factor (activated)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 10-pr-1985 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
 C;Accession: S45281; A61329
 R;Shibuya, Y.; Sembra, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
 Biochim. Biophys. Acta 1206, 63-70, 1994
 A;Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human Hageman factor. PMID:8186281
 A;Accession: S45281
 A;Molecule type: mRNA
 A;Residues: 1-593 <SH1>
 A;Cross references: GB:S70164
 A;Note: The authors Translated the codon GAG for residue 23 as Val, GAG for residue 70 as Glu, Pro, CTC for residue 203 as Phe, CTC for residue 247 as Leu, CCG for residue 286 as Glu, and ATC for residue 505 as Leu
 R;Fujikawa, K.; Walsh, K.A.; Davie, E.W.
 Biochemistry 16, 2270-2278, 1977
 A;Title: Isolation and characterization of bovine factor XII (Hageman Factor).
 A;Reference number: A61329; PMID:77182112;
 A;Accession: A61329
 A;Molecule type: protein
 A;Residues: 10-16,'X',18-19,525-550 <FUJ>
 C;Superfamily: coagulation factor XII; BGP homology; fibronectin type I repeat homology
 C;Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma; e
 P;37-79/Domain: fibronectin type II repeat homology <1P2>
 P;8-120/Domain: BGP homology <BCP>
 P;125-160/Domain: fibronectin type I repeat homology <FB1>
 P;207-287/Domain: kringle homology <TRY>
 P;541/Active site: Ser #status predicted

Query Match 5.2%; Score 13; DB 2; Length 593;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQGDGGPLVC 206
 Db 535 DACQGDGGPLVC 547

RESULT 11

S28941 coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
 N;Alternate names: Hageman factor
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 R;Sembra, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
 Biochim. Biophys. Acta 1159, 111-121, 1992
 A;Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage site

A;Reference number: S28941; MUID:93003367; PMID:1390917
 A;Accession: S28941
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-603 <SEM>
 A;Cross-references: EMBL:X66615; NID:949578; PID:CAA48600_1; PID:949579
 C;Superfamily: coagulation factor XII; BGP homology; fibronectin type I repeat homology
 C;Keywords: hydrolase; serine protease
 P;16-87/Domain: fibronectin type II repeat homology <FB1>
 P;134-169/Domain: fibronectin type I repeat homology <FB1>
 P;177-208/Domain: BGP homology <BGP>
 P;216-234/Domain: kringle homology <KRG>
 P;359-597/Domain: trypsin homology <TRY>
 Query Match 5.2%; Score 13; DB 2; Length 603;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQGDGGPLVC 206
 Db 545 DACQGDGGPLVC 557

RESULT 12

KFNU12 coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human
 N;Alternate names: Hageman Factor (activated)
 C;Species: Homo sapiens (man)
 C;Date: 27-Nov-1985 #sequence_revision 30-Jun-1991 #text_change 08-Dec-2000
 C;Accession: A29411; A26811; A00930; A25191; A22248; A21037
 R;Cool, D.E.; MacGillivray, R.T.A.
 J. Biol. Chem. 262, 13662-13673, 1987
 A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon 9
 A;Accession: A29411; MUID:88007593; PMID:2887862
 A;Molecule type: DNA
 A;Residues: 1-615 <COO>
 A;Cross-references: GB:MM17466; GB:J02807; NID:94959490_1; PID:9180357
 R;Tripathi, M.; Citarella, F.; Guida, S.; Gallelli, P.; Pantoni, A.; Cortese, R.
 Nucleic Acids Res. 14, 3146, 1986
 A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).
 A;Reference number: A26814; PMID:86176794; PMID:3754331
 A;Accession: A26814
 A;Molecule type: mRNA
 A;Residues: 4-615 <TRI>
 A;Cross-references: GB:MM1315; NID:9182291; PID:AAA70225_1; PID:9180358; PID:9180358
 R;Que, B.G.; Davie, B.W.
 Biochemistry 25, 1525-1528, 1986
 A;Title: Characterization of a cDNA coding for human factor XII (Hageman Factor).
 A;Accession: A25191; MUID:86216049; PMID:3011063
 A;Accession: A25191
 A;Molecule type: mRNA
 A;Residues: 14-312, 'S', 334-615 <CO2>
 A;Cross-references: GB:MM1723; NID:9180358; PID:9180358
 R;Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.
 J. Biol. Chem. 260, 13666-13676, 1985
 A;Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the
 A;Reference number: A00930; MUID:86033830; PMID:3877053
 A;Accession: A00930
 A;Molecule type: mRNA
 A;Residues: 14-312, 'S', 334-615 <CO2>
 A;Cross-references: GB:MM1723; NID:9180358; PID:9180358
 R;Que, B.G.; Davie, B.W.
 Biochemistry 25, 1525-1528, 1986
 A;Title: Characterization of a cDNA coding for human factor XII (Hageman Factor).
 A;Accession: A25191
 A;Molecule type: mRNA
 A;Residues: 146-378, 'G', 380-615 <QUB>
 A;Cross-references: GB:MM13147; NID:9180360; PID:9180360
 R;McMullan, B.A.; Fujikawa, K.
 J. Biol. Chem. 260, 5328-5341, 1985
 A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated H_a)
 A;Reference number: A22248
 A;Molecule type: protein
 A;Residues: 20-379 <MCM>
 R;Fujikawa, K.; McMullan, B.A.
 J. Biol. Chem. 258, 10924-10933, 1983
 A;Title: Amino acid sequence of human beta-factor XIIa.
 A;Reference number: A21037; MUID:83291041; PMID:6604055

A;Accession: A21037
A;Molecule type: protein-615 <FUJ>
R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucose is present in the first epidermal growth factor domain of facto
A;Reference number: A44606; MUID:92184750; PMID:1544894
A;Contents: annotation; carbohydrate binding site
C;Genetics:
A;Gene: GDB:F12
A;Cross-references: GDB:119892; OMIM:234000
A;Map Coordinates: 5q34-5qter
A;Introns: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/
C;Complex: Factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic
C;Function:
A;Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma kinin
A;Pathway: blood coagulation; fibrinolysis
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle; plasma; e
P;1-19/Domain: signal sequence #status predicted <S1G,
P;2-372-373-615/Product: coagulation factor XIIa, alpha form #status experimental <A12,>
P;47-88/Domain: fibronectin type II repeat homology <FB2>
P;98-130/Domain: EGF homology <EG1,>
P;135-170/Domain: fibronectin type I repeat homology <FN1>
P;178-209/Domain: EGF homology <EG2,>
P;211-295/Domain: kringle homology <KRG>
P;298-356/Region: proline-rich
P;354-362-373-615/Product: coagulation factor XIIa, beta form #status experimental <B12>
P;373-609/Domain: trypsin homology <TRY>
P;98-110; 104-119; 121-130; 135-163; 161-170; 178-189; 183-198; 200-209; 217-295; 238-277; 266-290
P;109/Binding site: carbohydrate (Thr) (covalent) #status experimental
P;249, 433/Binding site: carbohydrate (Asn) (covalent) #status experimental
P;299, 305, 329, 337/Binding site: carbohydrate (Thr) (covalent) #status predicted
P;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
P;412, 461, 563/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A;Accession: S65465
A;Molecule type: mRNA
A;Cross-references: EMBL:X94691; NID:91177315; PID:91177316
A;Residues: 1-254
A;Accession: S65403
A;Molecule type: protein
A;Cross-references: EMBL:X94691
A;Residues: 27-36 <B0W>
A;Note: 27-Leu, 35-Leu were also found
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
P;1-16/Domain: signal sequence #status predicted <SIG>
P;17-26/Domain: propeptide #status predicted <PRO>
P;27-254/Product: trypsin #status experimental <PAT>
P;27-247/Domain: trypsin homology <TRY>
P;53-69, 154-158, 195-238, 204-228/Disulfide bonds: #status predicted
P;68-113-208/Active site: His, Asp, Ser #status predicted

RESULT 13
T30337
Polyprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
Submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from Xe
A;Accession: T30337
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-1524 <YAN>
A;Cross-references: EMBL:U81290; NID:g2981640; PID: AAC24717.1
C;Superfamily: tyrosin related polypeptide; trypsin homology

Query Match 5.2%; Score 13; DB 2; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A;Accession: 194 DACQDGSGGPLV 206
A;Accession: 202 DACQDGSGGPLV 213

Search completed: June 16, 2004, 15:15:32
Job time : 21 secs

RESULT 14
Qy 194 DACQDGSGGPLV 206
Db 762 DACQDGSGGPLV 774

protein - protein search, using sw model	GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.	Search time 17 Seconds (without alignments) 759.612 Million cell updates/sec	P35041 anophelis g P35035 anophelis g P35037 anophelis g P35038 anophelis g P35036 anophelis g P35030 drosoiphila P354630 drosoiphila Q9ubx7 homo sapien Q9ubz3 homo sapien Q9ukq9 homo sapien Q9ubx7 homo sapien Q9p0g3 homo sapien	
score:	248	US-10-006-116A-194		
oring table:	OLIGO Gapop 60.0 , Gapext 60.0			
quence:	1 MGISIIFULLCVLGLSQATP.GVTYICKYVWDWIRMMRNN 248			
database :	SwissProt_42::			
arched:	141681 seqs, 52070155 residues			
rd size :	0			
total number of hits satisfying chosen parameters:	141681			
minimum DB seq length: 0				
maximum DB seq length: 2000000000				
st-processing: Listing first 45 summaries				
SUMMARIES	%	Query Match Length DB ID	Description	
Bult No.	Score			
1	248	100.0	KURC_HUMAN	O9ukr0 homo sapien
2	13	5.2	CPAD_HUMAN	P07146 homo sapien
3	13	5.2	URTG_DESRO	P49150 desmodus ro
4	13	5.2	URTB_DESRO	P98121 desmodus ro
5	13	5.2	TMS5_MOUSE	O9er04 mus musculu
6	13	5.2	TMS5_HUMAN	Q9hs3s3 homo sapien
7	13	5.2	URTL_DESRO	P98119 desmodus ro
8	9	5.2	URT2_DESRO	P15638 desmodus ro
9	13	5.2	TPA_MOUSE	P11214 mus musculu
10	13	5.2	TPA_RAT	P196317 rattus norv
11	13	5.2	TPA_HUMAN	P00750 homo sapien
12	13	5.2	TPA_BOVIN	Q28198 bos taurus
13	13	5.2	FA12_BOVIN	P98140 bos taurus
14	13	5.2	FA12_CAVIO	Q04962 cavia porce
15	13	5.2	FA12_HUMAN	P00748 homo sapien
16	13	5.2	HGFA_MOUSE	O9ri98 mus musculu
17	13	5.2	TMS6_HUMAN	Q8i180 homo sapien
18	13	5.2	TMS6_MOUSE	Q9db10 mus musculu
19	12	4.8	KLK6_HUMAN	Q92B76 homo sapien
20	12	4.8	FA12_BOVIN	P54625 drosophila
21	12	4.8	FA12_HUMAN	P54626 drosophila
22	12	4.8	TRYD_DROME	P42276 drosophila
23	12	4.8	TRYD_DROME	P42277 drosophila
24	12	4.8	TRYP_SARBU	P51588 sarcophaga
25	12	4.8	HYPB_HYPLI	P35588 hypoderma 1
26	12	4.8	TRYB_DROER	P54624 drosophila
27	12	4.8	TRYA_DROER	P04B14 drosophila
28	12	4.8	TRYE_DROER	P54627 drosophila
29	12	4.8	TRYF_DROER	P35005 drosophila
30	12	4.8	TRYU_DROER	P54629 drosophila
31	12	4.8	CPAD_PIG	P51779 sus scrofa
32	12	4.8	TRYV_DRONM	P42279 bombyx mori
33	12	4.8	VDP_BOMMO	O07943 bombyx mori

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CC	SEQUENCE	RESULT 2
CC	CPAD_HUMAN	CPAD_HUMAN
CC	ID_CPAD_HUMAN	STANDARD;
CC	P00746;	PRT;
CC	DT 21-JUL-1986 (Rel. 01, Created)	AC
CC	DT 15-DEC-1998 (Rel. 37, Last sequence update)	DT
CC	DT 15-MAR-2004 (Rel. 43, Last annotation update)	DT
CC	DB Complement factor D precursor (EC 3.4.21.46) (C3 convertase activator)	DB
CC	DB (Properdin factor D) (Adipsin).	DB
DR	DR Homo sapiens (Human).	GN
EMBL; AF135025; AAF06065..1; .	OS	
DR	DR Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; .	OC
EMBL; AC011473; AAG23258..1; .	OC	
DR	DR Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. .	OC
HSSP; P00763; IBDP0.	NCBI_TaxID=9606;	OX
DR	[1] _TaxID=9606;	RN
DR	DR RN	RN
DR	DR SEQUENCE OF 8-253 FROM N.A.	RP
DR	DR GO:0005576; C: extracellular; NAS.	RX
DR	DR GO:0004252; F: serine-type endopeptidase activity; NAS.	RX
DR	DR GO:0005508; P: proteolysis; NAS.	RA
DR	DR InterPro; IPR003003; Cys_Ser_trypsin.	RA
DR	DR InterPro; IPR001254; Peptidase_S1.	RA
DR	DR InterPro; IPR001314; Peptidase_S1A.	RT
DR	DR Pfam; PF00089; trypsin; 1.	RT
DR	DR PRINTS; PR00722; CHYMOTRYPSIN.	RT
DR	DR SMART; SM00000; TRYSP_SPC; 1.	RT
DR	DR PROSITE; PS50240; TRYPsin DOM; 1.	RT
DR	DR PROSITE; PS00134; TRYPsin HIS; 1.	RT
DR	DR PROSITE; PS00135; TRYPsin SER; 1.	RT
KW	KW Hydrolase; Serine protease; Glycoprotein; Signal;	RT
FT	FT SIGNAL 1 17	RT
FT	FT ALTERNATIVE splicing.	RT
FT	FT CHAIN 18 248	RT
FT	FT ACT SITE 62 62	RL
FT	FT ACT-SITE 108 108	RL
FT	FT ACT SITE 200 200	RL
FT	FT DISULFID 28 161	RL
FT	FT DISULFID 47 63	RL
FT	FT DISULFID 133 235	RL
FT	FT DISULFID 140 206	RL
FT	FT DISULFID 172 186	RL
FT	FT DISULFID 196 222	RL
FT	FT CARBONYL 24 24	RL
FT	FT CARBONYL 163 163	RL
FT	FT VARSPLIC 236 248	RL
SQ	SQ SEQUENCE 248 AA; 26733 MW; BB473B98P8BAF703 CRC64;	RP
Qy	Qy Query Match 100.0%; Score 248; DB 1; Length 248;	RP
Db	Db Best Local Similarity 100.0%; Pred. No. 7.9e-255; Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RP
Qy	Qy 1 MGISIPLLCLVGLSQATPKLNGTEGRNSQPWQGLFEGTSRCGVLDHRVLTAA 60	RP
Db	Db 1 MGISIPLLCLVGLSQATPKLNGTEGRNSQPWQGLFEGTSRCGVLDHRVLTAA 60	RP
Qy	Qy 61 AHCGSGSRWVRLGEHSLSQLDTEQIRHSGFVTHPEYLGASTSHEDLRLRLRLPVRY 120	RP
Db	Db 61 AHCGSGSRWVRLGEHSLSQLDTEQIRHSGFVTHPEYLGASTSHEDLRLRLRLPVRY 120	RP
Qy	Qy 121 TSSVQPLPNDCATACTECHVSGWGTINHPNPANPPDQLQCLNLISIVSATCHGVYGR 180	RP
Db	Db 121 TSSVQPLPNDCATACTECHVSGWGTINHPNPANPPDQLQCLNLISIVSATCHGVYGR 180	RP
Qy	Qy 181 TSNMVCAGGVPGQDAGQDGSQGPVLVCGVLOGLSVSQPGQDGIPGVTYICKYVDW 240	RP
Db	Db 181 TSNMVCAGGVPGQDAGQDGSQGPVLVCGVLOGLSVSQPGQDGIPGVTYICKYVDW 240	RP
Qy	Qy 241 IRMIMRN 248	RP
Db	Db 241 IRMIMRN 248	RP
Qy	Qy "Structure of human factor D. A complement system protein at 2.0-A resolution."	RT
Db	Db J. Mol. Biol. 235:655-708 (1994).	RL
Qy	Qy [9]	RN
Db	Db X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).	RP
Qy	Qy X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).	RP
Db	Db MEDLINE=901118317; PubMed=8289289;	RX
Qy	Qy 121 Narayana S.V.L., Carlson M., El-Kabbani O., Kilpatrick J.M., Moore D., Chen X., Bugg C.E., Volanakis J.E., DeLucas L.J.;	RA
Db	Db Proc. Natl. Acad. Sci. U.S.A. 77:4938-4942 (1980).	RA
Qy	Qy [8]	RA
Db	Db X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).	RP
Qy	Qy MEDLINE=81054856; PubMed=6776531;	RX
Db	Db "Active site amino acid sequence of human factor D.";	RA
Qy	Qy [1]	RA
Db	Db Proc. Natl. Acad. Sci. U.S.A. 77:1116-1119 (1980).	RA
Qy	Qy [7]	RA
Db	Db PARTIAL SEQUENCE OF 26-78.	RP
Qy	Qy PARTIAL SEQUENCE OF 26-51 AND 194-220.	RP
Db	Db PARTIAL SEQUENCE OF 26-51; PubMed=821372;	RX
Qy	Qy PARTIAL SEQUENCE OF 26-51; PubMed=825615;	RA
Db	Db Johnson D.M.A., Gagnon J., Reid K.B.M.; "Amino acid sequence of human factor D of the complement system.	RA
Qy	Qy Johnson D.M.A., Gagnon J., Reid K.B.M.; "Amino acid sequence of human D of the alternative complement pathway."	RA
Db	Db Johnson D.M.A., Gagnon J., Reid K.B.M.; "Amino acid sequence of human factor D and proteases of non-plasma origin."	RA
Qy	Qy Johnson D.M.A., Gagnon J., Reid K.B.M.; "Factor D of the alternative pathway of human complement.	RA
Db	Db Purification, alignment and N-terminal amino acid sequences of the major cyanogen bromide fragments, and localization of the serine residue at the active site."	RA
Qy	Qy [6]	RA
Db	Db Biochem. J. 187:863-874 (1980).	RL
Qy	Qy [5]	RA
Db	Db FBBS Lett. 166:347-351 (1984).	RA
Qy	Qy [4]	RA
Db	Db PARTIAL SEQUENCE OF 26-252.	RP
Qy	Qy PARTIAL SEQUENCE OF 26-51; PubMed=633133;	RP
Db	Db MEDLINE=84108930; PubMed=633133;	RX
Qy	Qy [3]	RA
Db	Db "Amino acid sequence of human factor D of the complement system.	RA
Qy	Qy [2]	RA
Db	Db Niemann M.A., Bhown A.S., Bennett J.C., Volanakis J.E.; "Amino acid sequence of human D of the alternative complement pathway."	RA
Qy	Qy [1]	RA

RX	MEDLINE=96025634; PubMed=7592653;	Q -> G (IN REF. 4).
RA	Kim S., Narayana S.V., Volanakis J.E.;	TCNRPFHDAITE -> KCRLYDVL (IN REF. 4).
RT	"Crystal structure of a complement factor D mutant expressing enhanced catalytic activity".	S -> T (IN REF. 3).
RL	J. Biol. Chem. 270:24399-24405 (1995).	S -> H (IN REF. 3).
CC	-I- FUNCTION: Factor D cleaves factor B when the latter is complexed with factor C3b, activating the C3bb complex, which then becomes homologous to that of C3s in the classical pathway. Its function is	MISSING (IN REF. 4).
CC	the C3 convertase of the alternate pathway. Its function is	
CC	homologous to that of C3s in the classical pathway.	
CC	-I- CATALYTIC ACTIVITY: Cleaves component factor B (Arg- -Lys) when in complex with C3b or with cobra venom factor (CVF).	
CC	-I- SIMILARITY: Belongs to peptidase family S1.	
CC	-I- CAUTION: In addition to the conflicts shown in the feature table, Ref.3 sequence had a peptide in the wrong order and another one missing.	
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CC	EMBL: AAA4526; DR: PIR: A40197; DBHU: MBR05; S01.197; ALT_INIT.	
DR	PDR: 1DPP; 25-FEB-98.	
DR	PDB: 1DST; 11-JUL-98.	
DR	PDB: 1DSU; 17-AUG-96.	
DR	PDB: 1BIO; 22-JUN-99.	
DR	PDB: 1DIC; 22-JUL-99.	
DR	PDB: 1FDP; 03-DBC-99.	
DR	PDB: 1HFD; 22-JUN-99.	
DR	MEROPS: S01.197; -.	
DR	Genew: HENG:2771; DF.	
DR	MIM: 134350; -.	
DR	GO: GO:0003B17; P: complement factor D activity; TAS.	
DR	GO: GO:0008236; P: serine-type peptidase activity; TAS.	
DR	GO: GO:0006956; P: complement activation; TAS.	
DR	GO: GO:0006508; P: proteolysis and peptidolysis; TAS.	
DR	InterPro: IPR009003; Cys Ser trypsin.	
DR	InterPro: IPR001254; Peptidase_S1.	
DR	InterPro: IPR001314; Peptidase_S1A.	
DR	Pfam: PF000089; trypsin; 1.	
DR	PRINTS: PR00722; CHYMOTRYPSIN.	
DR	SMART: SM00020; TRYSP_SPC_1.	
DR	PROSTTB: PS50240; TRYPSIN_DOM; 1.	
DR	PROSTTB: PS00134; TRYPSIN_HIS; 1.	
DR	PROSTTB: PS00135; TRYPSIN_SER; 1.	
KW	Complement alternate pathway; Plasma; Hydrolase; Serine protease; Zymogen; Glycoprotein; Signal; 3D-structure.	
FT	SIGNAL 1 20 POTENTIAL.	Score 13; DB 1; Length 253;
FT	PROPER 21 25 ACTIVATION PEPTIDE (POTENTIAL).	Best Local Similarity 100.0%; Pred. No. 6.8e-06; Mismatches 0; Indels 0; Gaps 0;
FT	CHAIN 26 253 COMPLEMENT FACTOR D.	
FT	ACT SITE 66 66 CHARGE RELAY SYSTEM.	
FT	ACT SITE 112 112 CHARGE RELAY SYSTEM.	
FT	ACT SITE 208 208 CHARGE RELAY SYSTEM.	
FT	DISULFID 51 67 DESTR0	RESULT 3
FT	DISULFID 148 214 DESTR0	URTG DESTR0
FT	DISULFID 179 195 DESTR0	ID _URTG DESTR0
FT	DISULFID 204 229 STANDARD,	AC P49150;
FT	CONFICT 26 26 DT 01-PTR-1996 (Rel. 33, Created)	
FT	CONFICT 35 35 DT 01-PTR-1996 (Rel. 33, Last sequence update)	
FT	CONFICT 40 40 DT 28-PTR-2003 (Rel. 41, Last annotation update)	
FT	CONFICT 49 49 DT Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA gamma).	
FT	CONFICT 52 52 OS Desmodus rotundus (Vampire bat).	
FT	CONFICT 59 59 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Rutheria; Chiroptera; Microchiroptera; Phyllostomidae; Desmodontinae; Desmodus.	
FT	CONFICT 63 63 OC	
FT	CONFICT 73 73 OC	
FT	CONFICT 83 86 OC	
FT	CONFICT 83 84 OC	
FT	CONFICT 94 95 OC	
FT	CONFICT 96 96 OC	

OX NCBI_TaxID=9430;	PT DISULFID 341 369 BY SIMILARITY.
RN [1] SEQUENCER FROM N.A.	PT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
RP TISSUE=Salivary gland;	PT SEQUENCE 394 AA; 44105 MW; 9CCD6F52F3DB8FC0 CRC64 ;
RX MEDLINE=9203016; PubMed=1937019;	Query Match 5.2%; Score 13; DB 1; Length 394;
RA Kraetzschmar J.; Haendler B.; Langer G.; Boidol W.; Bringmann P.,	Best Local Similarity 100.0%; Pred. No. 1e-05;
RA Alagon A.; Donner P.; Schleuning W.D.;	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RT "The plasminogen activator family from the salivary gland of the	
RT vampire bat Desmodus rotundus: cloning and expression.";	
RL Gene 105:229-237(1991).	
RN [2]	
RP CHARACTERIZATION.	
RX MEDLINE=93393059; PubMed=1309059;	RESULT 4
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,	URTB DBSRO STANDARD: PRT: 431 AA.
RA Kraetzschmar J., Haendler B., Langer G., Baidus B., Witt W.,	ID URTB DBSRO
RA Donner P.	AC P9821;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common	AC 01-PBB-1996 (Rel. 33, Created)
RT vampire bat): unique fibrin specificity.";	DT 01-PBB-1996 (Rel. 33, Last sequence update)
RL Ann. N.Y. Acad. Sci. 667:395-403 (1992).	DT 01-PBB-1996 (Rel. 41, Last annotation update)
CC -I- FUNCTRION: Probably essential to support the feeding habits of this	DB Salivary plasminogen activator beta precursor (BC 3.4.21.68) (DSPA
CC exclusively haemophagous animal. Probable potent thrombolytic	agent.
CC agent.	DB Desmodus rotundus (Vampire bat).
CC -I- CATALYTIC ACTIVITY: Specific cleavage of Arg- -val bond in	OS Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC plasminogen to form plasmin.	OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
CC -I- SUBUNIT: Monomer.	OC Desmodontinae; Desmodus.
CC -I- SIMILARITY: Belongs to peptidase family S1.	NCBI TaxID=9410;
CC -I- SIMILARITY: Contains 1 kringle domain.	OX
CC	RN [1]
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between the Swiss Institute of Bioinformatics and the EMBL outstation -	RX MEDLINE=93393059; PubMed=1309059;
the European Bioinformatics Institute. There are no restrictions on its	RC SEQUENCE FROM N.A.
use by non-profit institutions as long as its content is in no way	RC TISSUE=Salivary gland;
modified and this statement is not removed. Usage by and for commercial	RC MEDLINE=9203016; PubMed=1937019;
entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RA Kraetzschmar J.; Haendler B.; Langer G.; Boidol W., Bringmann P.,
CC	RA Donner P.;
CC	RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
CC	RA Baidus B., Witt W.,
CC	RA "Plasminogen activators from the saliva of Desmodus rotundus (common
CC	RT vampire bat): unique fibrin specificity.";
CC	RA Ann. N.Y. Acad. Sci. 667:395-403 (1992).
CC	CC -I- FUNCTION: Probably essential to support the feeding habits of this
CC	CC exclusively haemophagous animal. Probable potent thrombolytic
CC	CC agent.
CC	CC -I- CATALYTIC ACTIVITY: Specific cleavage of Arg- -val bond in
CC	CC plasminogen to form plasmin.
CC	CC -I- SUBUNIT: Monomer.
DR PIR: JS0600; JS0600.	CC -I- SIMILARITY: Belongs to peptidase family S1.
DR HSSP: PP8119; 1A51.	CC -I- SIMILARITY: Contains 1 RGP-like domain.
DR InterPro: IPR009003; Cys Ser trypsin.	CC -I- SIMILARITY: Contains 1 kringle domain.
DR InterPro: IPR000001; Kringle.	CC
DR InterPro: IPR001254; Peptidase_S1.	CC
DR InterPro: IPR001314; Peptidase_SIA.	CC
DR Pfam: PF00051; kringle_1.	CC
DR Pfam: PF00089; trypsin_1.	CC
DR PRINTS: PR0072; CHYMOTRYPSIN.	CC
DR PRINTS: PR00018; KRINGLE.	CC
DR PRODom: PD000395; kringle_1.	CC
DR SMART: SM00130; KR_1.	CC
DR SMART: SM00020; TRYD_SPC_1.	CC
DR PROSITE: PS00021; KRINGLE_1; 1.	CC
DR PROSITE: PS50070; KRINGLE_2; 1.	CC
DR PROSITE: PS50240; TRYPSIN_DOM; 1.	CC
DR PROSITE: PS00134; TRYPSIN_HIS; 1.	CC
DR PROSITE: PS00135; TRYPSIN_SER; 1.	CC
KW Plasminogen activation: Hydrolyse; Serine protease; Glycoprotein; Kringle; Signal; Multigene family.	CC
RW SIGNAL 1 36 POTENTIAL.	CC
PT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.	CC
PT DOMAIN 45 126 KRINGLE.	CC
PT DOMAIN 142 394 SERINE PROTEASE.	CC
PT ACT SITE 189 189 CHARGE RELAY SYSTEM (BY SIMILARITY).	CC
PT ACT SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).	CC
PT ACT SITE 345 345 BY SIMILARITY.	CC
PT DISULFID 45 126 BY SIMILARITY.	CC
PT DISULPID 66 108 BY SIMILARITY.	CC
PT DISULPID 97 121 BY SIMILARITY.	CC
PT DISULFID 131 262 BY SIMILARITY.	CC
PT DISULFID 174 190 BY SIMILARITY.	CC
PT DISULFID 182 251 BY SIMILARITY.	CC
PT DISULFID 276 351 BY SIMILARITY.	CC
PT DISULFID 308 324 BY SIMILARITY.	CC
DR PIR: JS0599; JS0599.	DR EMBL; MG3989; ARAB1594_1; -.
DR HSSP: PP8119; 1A51.	DR PIR: JS0599; JS0599.
DR MEROPS; 80_239; -.	DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; RGP like.	DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.	DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_SIA.	DR InterPro; IPR001314; Peptidase_SIA.

RESULT 6						
	VARSPLIC	183	192	GGLYVEEAKRP → MBAQVGLLNV (in isoform 1).		
FFT	CONFFLICT	325	325	/PfId=VSP 0051398.		
FFT	SEQUENCE	455 AA;	49632 MW;	D → G (IN PRF. 1; BA020277).		
SQ				5CFC31789C8899AA CR064;		
	Query Match	5.2%	Score 13;	DB 1; Length 455;		
	Best Local Similarity	100.0%	Pred. No. 1.2e-05;			
	Matches	13;	Conservative	Mismatches 0;	Indels 0;	Gaps
Qy	194	DACOGDGGAGPLVC 206				
Dbs	399	DACOGDGGAGPLVC 411				
	TMTN55_HUMAN	TMTN55_HUMAN	STANDARD;	PRT;	457 AA.	
	Q9H3S3;					
	AC					
	DT	16-OCT-2001 (Rel. 40, Created)				
	DT	16-OCT-2001 (Rel. 40, Last sequence update)				
	DT	28-FEB-2003 (Rel. 41, Last annotation update)				
	DT	Transmembrane protease, serine 5 (EC 3.4.21.-) (spinesin).				
	GN	TMFRSS5.				
	OS	Homo sapiens (Human)				
	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;				
	NCBI_TaxID	9606;				
	DX					

QUENCE FROM N.A.
SUBCELLULAR LOCATION: Brain;
ISSUE=Brain;
SOURCE=Brain;
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in neurons, in their axons, and at the synapses of motoneurons in the spinal cord.
SIMILARITY: Belongs to peptidase family S1.
SIMILARITY: Contains 1 SSCR domain.

ISSUE=Brain;
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in neurons, in their axons, and at the synapses of motoneurons in the spinal cord.

ISSUE=Brain;
SUBCELLULAR LOCATION: Type II membrane protein (Potential).
TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in neurons, in their axons, and at the synapses of motoneurons in the spinal cord.

AB028140; BAB20375.1; - .
 SP; P00763; 1DPO.
 new; HGNC:14908; TMRSS5.
 4; 606751; - .
 Q9CPS; S01_313; - .
 terPro; IPK009003; Cys Ser trypsin.
 terPro; IPK001254; Peptidase_S1.
 terPro; IPK001314; Peptidase_SIA.
 terPro; IPK001130; Srrc receptor.
 MNTS; PR0022; CHYMOTRYPsin.
 ARTI; SM002020; TRYPSIN; 1.
 DISITE; PS50240; TRYPSIN DOM; 1.
 DISITE; PS00134; TRYPSIN HIS; 1.
 DISITE; PS00135; TRYPSIN SER; 1.
 DISITE; PS00420; SRCR 1; FALSE NEG.
 DISITE; PS50287; SRCR 2; FALSE NEG.
 tirolase; Serine protease; Transmembrane; Signal-anchor;
 coprotein.
 MAIN 1 49 CYTOPLASMIC (POTENTIAL).
 ANSMEM 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 MAIN 71 457

RESULT	7	URTI	DBSRO	STANDARD:	PRT:	477 AR.
		AC	P98119;			
		AC	01-PFB-1996	(Rel. 33, Created)		
		DT	01-PFB-1996	(Rel. 33, Last sequence update)		
		DT	01-MAR-2004	(Rel. 43, Last annotation update)		
		DB	Salivary plasminogen activator alpha 1 precursor			
		DS	Desmodus rotundus ('Vampire bat')			
		DS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata			
		OC	Mammalia; Metazoa; Chiroptera; Microchiroptera			
		OC	Desmodontinae; Desmodontidae			
		OC				

OX NCBI_TaxId:9430;

[1] RN RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Gland;
RX MEDLINE=9039056; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
RA Agon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
vampire bat *Desmodus rotundus*: cloning and expression.";
RL Gene 105:229-237(1991).
[2] RN RP CHARACTERIZATION.
RX MEDLINE=9393055; PubMed=1309055;
RA Schleuning W.-D., Agon A., Boidol W., Bringmann P., Petri T.,
RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
RA Donner P.,
RT "Plasminogen activators from the saliva of *Desmodus rotundus* (common
vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
[3] RN RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RC TISSUE=Salivary Gland;
RX MEDLINE=98022741; PubMed=9354616;
RA Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
RA Schleuning W.D., Bode W.;
RT "Catalytic domain structure of vampire bat plasminogen activator: a
molecular paradigm for proteolytic without activation cleavage.";
RA Biochemistry 36:13483-13493(1997).
RL CC -!
CC -!- FUNCTION: Probably essential to support the feeding habits of this
exclusively haemophagous animal. Potent thrombolytic agent.
CC -!
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg | -Val bond in
plasminogen to form plasmin.
CC -!

-|- ENZYME REGULATION: Activity toward plasminogen is stimulated in
CC the presence of fibrin I.
CC -|- SUBUNIT: Monomer.
CC -|- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
CC and the kringle domain apparently mediates fibrin-induced
CC stimulation of activity.
CC -|- SIMILARITY: Belongs to Peptidase family S1.
CC -|- SIMILARITY: Contains 1 IgGF-like domain.
CC -|- SIMILARITY: Contains 1 fibronectin type I domain.
CC -|- SIMILARITY: Contains 1 kringle domain.

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DR EMBL; M63987; AAA31591_1;
DR EMBL; M63986; AAA31592_1;
DR PIR; JS0597;
DR PDB; 1ASI; 23-MAR-99.
DR MEROPS; S01_232; -.
DR Glycoquery; P88119; -.
DR InterPro; IPR005003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGFR-like.
DR InterPro; IPR000083; Fibronectin.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; BGP_1.
DR Pfam; PF00039; Eni_1.
DR Pfam; PF00051; Kringle_1.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PRO00722; CHYMOTRYPSIN.
DR PRINTS; PRO00018; KRINGLE.
DR Prodrom; PD000395; Kringle_1.
DR SMART; SM00181; EGFR_1.
DR SMART; SM00058; FN1_1.
DR SMART; SM00130; KR_1.
DR SMART; SM00020; TRYSPC_1.
DR PROSITE; PS000022; BGP_1.
DR PROSITE; PS01186; BGP_2; 1.
DR PROSITE; PS00026; BGP_3; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRIPSIN_DOM; 1.
DR PROSITE; PS00134; TRIPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Plasminogen activation: Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGFR-like domain; Signal Multigene family; 3D-structure.
FT SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 477 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1.
FT DOMAIN 40 82 FIBRONECTIN TYPE-I.
FT DOMAIN 83 121 BGP-LIKE.
FT DOMAIN 128 209 KRINGLE.
FT DOMAIN 225 477 SPRINE PROTEASE.
FT ACT SITE 321 321 CHARGE RELAY SYSTEM.
FT ACT SITE 428 428 CHARGE RELAY SYSTEM.
FT DISULFID 42 72 BY SIMILARITY.
FT DISULFID 70 79 BY SIMILARITY.
FT DISULFID 87 98 BY SIMILARITY.
FT DISULFID 92 109 BY SIMILARITY.
FT DISULFID 111 120 BY SIMILARITY.
FT DISULFID 128 203 BY SIMILARITY.
FT DISULFID 149 191 BY SIMILARITY.
FT DISULFID 180 204 BY SIMILARITY.
FT DISULFID 214 345 BY SIMILARITY.
FT DISULFID 257 273 BY SIMILARITY.

FT DISULFID 265 334 N-LINKED (GLCNAC. . .).
FT DISULFID 359 434 /PfId=CAR_000027.
FT DISULFID 391 407 N-LINKED (GLCNAC. . .).
FT CARBOHYD 153 153 /PfId=CAR_000028.
FT TURN 214 215
FT TURN 223 224
FT TURN 226 227
FT STRAND 230 231
FT HELIX 234 236
FT TURN 238 239
FT STRAND 240 245
FT STRAND 254 263
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FT HELIX 271 273
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FT STRAND 358 363
FT STRAND 366 366
FT STRAND 374 374
FT STRAND 379 385
FT HELIX 388 390
FT TURN 393 398
FT TURN 403 404
FT STRAND 405 409
FT TURN 425 426
FT STRAND 428 429
FT STRAND 431 436
FT TURN 437 438
FT STRAND 439 448
FT TURN 455 456
FT STRAND 459 463
FT HELIX 464 467
FT HELIX 468 474
SQ SEQUENCE 477 AA; 53616 MW; AA06FD1739C10B5B CRC64;
Query Match Score 13; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

Oy 194 DACQGDGGP1NC 206
Db 422 DACQGDGGP1NC 434

RESULT 8
URT2_DESRO
ID URT2_DESRO
AC P15638
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DS Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA
alpha-2) (BAT-PA) (I-plasminogen activator).
DB Desmodus rotundus (Vampire bat).
OS Buxarvota; Metaxoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Butheria; Chiroptera; Microchiroptera; Phyllostomidae;

OC	Desmodontinae; Desmodus.	
OX	NCBI_TAXID=9430;	
RN	[1] RP SEQUENCE FROM N.A.	
RC	TISSUE=Salivary gland;	
RX	MEDLINE=92039046; PubMed=1937019;	
RA	Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,	
RA	"The plasminogen activator family from the salivary gland of the vampire bat Desmodus rotundus: cloning and expression.",	
RT	vampire bat Desmodus rotundus: cloning and expression.",	
RL	Gene 105:229-237(1991).	
RN	[2] RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RC	TISSUE=Salivary gland;	
RX	MEDLINE=90036867; PubMed=2509450;	
RA	Gardelli S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,	
RA	Register R.B., Jacobs J.W., Dixon R.A.P., Friedman P.A.;	
RT	isolation, characterization, and cDNA cloning of a vampire bat salivary plasminogen activator.",	
JL	J. Biol. Chem. 264:17947-17952(1989).	
[3]	RP CHARACTERIZATION.	
RX	MEDLINE=93193059; PubMed=1309059;	
RA	Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,	
RA	Donner P.; Langer G., Baldus B., Witt W.,	
RA	"Plasminogen activators from the saliva of Desmodus rotundus (common vampire bat): unique fibrin specificity.",	
Ann. N.Y. Acad. Sci. 667:395-403(1992).		
CC	-!- FUNCTION: Probably essential to support the feeding habits of this exclusively haemophagous animal. Probable potent thrombolytic agent.	
CC	-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-l-val bond in plasminogen to form plasman.	
CC	-!- ENZYME REGULATION: Activity toward plasminogen is stimulated in the presence of fibrin I.	
CC	-!- SUBSTRATE: Monomer.	
CC	-!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin, and the kringle domain apparently mediates fibrin-induced stimulation of activity.	
CC	-!- SIMILARITY: Belongs to peptidase family S1.	
CC	-!- SIMILARITY: Contains 1 EGF-like domain.	
CC	-!- SIMILARITY: Contains 1 fibronectin type I domain.	
CC	-!- SIMILARITY: Contains 1 kringle domain.	
CC	-----	
DR	EMBL: M63988; AAA31593.1; -.	
DR	EMBL: J05082; AAA31596.1; -.	
DR	PIR: A34369; A34369.	
DR	PIR: JS0588; JS0598.	
DR	HSSP: P98119; IAS1.	
DR	MEPROS: S01-232; -.	
DR	InterPro: IPR009003; Cys_Ser_trypsin.	
DR	InterPro: IPR006209; EGF_Like.	
DR	InterPro: IPR006083; Fibronectin.	
DR	InterPro: IPR006210; IEGF.	
DR	InterPro: IPR00001; Kringle.	
DR	InterPro: IPR001254; Peptidase_S1.	
DR	InterPro: IPR001314; Peptidase_S1A.	
PFam	PF00018; EGP; 1.	
PFam	PF00039; Fnn; 1.	
PFam	PF00051; kringle; 1.	
DR	PF0089; trypsin; 1.	
DR	PRINTS: PR00722; CHYMOTRYPSIN.	
DR	PRINTS: PR00018; KRINGLE.	
DR	ProDom: PD00395; Kringle; 1.	
DR	SMART: SM00181; EGF; 1.	
DR	SMART: SM00058; FN1; 1.	
DR	SMART: SM00020; TRYD; SPC; 1.	
DR	PROSITE: PS00022; BCF_1; 1.	
DR	PROSITE: PS01186; BCF_2; 1.	
DR	PROSITE: PS50026; EGF_3; 1.	
DR	PROSITE: PS01233; FIBRONECTIN_1; 1.	
DR	PROSITE: PS00021; KRINGLE_1; 1.	
DR	PROSITE: PS50010; KRINGLE_2; 1.	
DR	PROSITE: PS50240; TRYPSIN_DOM; 1.	
DR	PROSITE: PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE: PS00135; TRYPSIN_SER; 1.	
KW	Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-Like domain; Signal; Multigene family.	
KW	POTENTIAL.	
FT	SIGNAL	1
FT	CHAIN	37
FT	DOMAIN	40
FT	DOMAIN	83
FT	DOMAIN	128
FT	DOMAIN	225
FT	ACT_SITE	272
FT	ACT_SITE	321
FT	ACT_SITE	428
FT	DISULFID	42
FT	DISULFID	70
FT	DISULFID	79
FT	DISULFID	87
FT	DISULFID	98
FT	DISULFID	109
FT	DISULFID	120
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FT	DISULFID	434
FT	DISULFID	359
FT	DISULFID	407
FT	DISULFID	424
FT	CARBONYL	185
FT	CARBONYL	398
FT	CONFLICT	403
FT	CONFLICT	417
FT	CONFLICT	435
SQ	SEQUENCE	477 AA; 53719 MW; 17186555C0B5077C CRC64;
Query	Match Score 13; DB 1; Length 477;	
Best	Local Similarity 100.0%; Pred. No. 1.2e-05;	
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	422 DACQDSGGPLVC 434	
RESULT 9		
TPA_MOUSE STANDARD		
ID - TPA_MOUSE		
AC P1124; Q91VP2;		
DT 01-JUL-1989 (Rel. 11, Created)		
DT 10-OCT-2003 (Rel. 42, Last sequence update)		
DT 15-APR-2004 (Rel. 43, Last annotation update)		
DB Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)		
DE (t-PA) (t-plasminogen activator).		
GN PLAT.		
OS Mus musculus (Mouse).		
OC Chordata; Craniata; Vertebrata; Buteleostomi;		
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;		
OC NCBI_TaxID=10950;		
RN [1]		
RP SEQUENCE FROM N.A.		
RX MEDLINE=8808703; PubMed=2826484;		
RK Rickles R.J., Darrow A.L., Strickland S.;		
RJ Molecular cloning of complementary DNA to mouse tissue plasminogen		

activator mRNA and its expression during F9 teratocarcinoma cell differentiation." J. Biol. Chem. 265:1563-1569(1988).

SEQUENCE FROM N.A.

TISSUE=Hammary gland;

MEDLINE=2382257; PubMed=12477932;

straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Wagner L., Schuler C.M., Schuler G.D., Altschul S.F., Collins F.S., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Raha S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., Boak S.A., McEwan P.J., McFerran K.J., Garcia A.M., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Manly D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Kettman M., Madden A., Rodrigues S., Sanchez A., Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimmwood J., Schmitz U., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) ..

--> FUNCTION: Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.

--> CATALYTIC ACTIVITY: Specific cleavage of Arg-| -Val bond in plasminogen to form plasmin.

--> SUBUNIT: Heterodimer of chain A and chain B held by a disulfide bond.

--> SUBCELLULAR LOCATION: Secreted; extracellular.

--> PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKRIN OR FACTOR XA.

--> MISCELLANOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.

--> SIMILARITY: Belongs to peptidase family S1.

--> SIMILARITY: Contains 1 EGF-like domain.

--> SIMILARITY: Contains 2 Kringle domains.

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EMBL; J03520; AAA04070.1; -.

DR EMBL; BC011256; ABH11256.1; -.

DR PIR; A2941; A2941.

DR HSSP; P00750; 1A5H.

DR MEROPS; S01_232; -.

DR InterPro; IPR006210; IEGP.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR001354; Peptidase_S1.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00039; fnl; 1.

DR Pfam; PF00051; kringle; 2.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PR00722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE. DR PRODom; PD000395; Kringle; 2.

DR SMART; SM00131; EGF; 1.

DR SMART; SM00059; KR; 2.

DR SMART; SM00020; Tryp_Ser; 1.

DR PROSITE; PS00122; EGF; 2; 1.

DR PROSITE; PS00121; KRINGLE; 1.

DR PROSITE; PS00120; KRINGLE; 1; 2.

DR PROSITE; PS50070; KRINGLE; 2; 2.

DR PROSITE; PS00140; TRYPSIN_DOMAIN; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Plasminogen activation; Hydrolase; Serine Protease; Glycoprotein; PROBLE.

KW Plasma; Kringle; EGF-like domain; Repeat; Signal.

KW PROTEIN; SIGNAL; 17

KW PROTEIN; CHAIN; 17

KW PROTEIN; CHAIN; 30

KW PROTEIN; CHAIN; 308

KW PROTEIN; CHAIN; 559

KW PROTEIN; CHAIN; 559

KW PROTEIN; CHAIN; 309

KW PROTEIN; CHAIN; 36

KW PROTEIN; CHAIN; 78

KW PROTEIN; CHAIN; 117

KW PROTEIN; CHAIN; 205

KW PROTEIN; CHAIN; 205

KW PROTEIN; CHAIN; 294

KW PROTEIN; CHAIN; 559

KW PROTEIN; CHAIN; 355

KW PROTEIN; CHAIN; 404

KW PROTEIN; CHAIN; 510

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KW PROTEIN; CHAIN; 75

KW PROTEIN; CHAIN; 94

KW PROTEIN; CHAIN; 105

KW PROTEIN; CHAIN; 116

KW PROTEIN; CHAIN; 205

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KW PROTEIN; CHAIN; 559 AA;

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KW PROTE

GN PLAT. Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
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 RN [2]
 RP RX
 SEQUENCE FROM N.A. PubMed=3148445;
 RA NY T.; Leonardsson G.; Hauch A.J.W.;
 RT "Cloning and characterization of a cDNA for rat tissue-type
 plasminogen activator.";
 RL DNA 7:671-677(1988).
 RP RX
 SEQUENCE FROM N.A. PubMed=2105315;
 RA Peng P.; Ohlsson M.; Ny T.;
 RT "The structure of the tATA-less rat tissue-type plasminogen activator
 gene. Species-specific sequence divergences in the promoter predict
 differences in regulation of gene expression.";
 RL J. Biol. Chem. 265:2022-2072(1990).
 CC :- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
 to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
 controlling Plasmin-mediated proteolysis, it plays an important
 role in tissue remodeling and degradation, in cell migration and
 many other physiopathological events.
 CC :- CATALYTIC ACTIVITY: Specific cleavage of Arg-| -val bond in
 plasminogen to form plasmin.
 CC :- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
 bond.
 CC :- SUBCELLULAR LOCATION: Secreted, extracellular.
 CC :- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC :- MISCELLANEOUS: Binds to the kringle structure of the fibrin A
 chain. Binding to fibrin enhances its catalytic activity.
 CC :- SIMILARITY: Belongs to peptidase family S1.
 CC :- SIMILARITY: Contains 1 EGF-like domain.
 CC :- SIMILARITY: Contains 1 fibronectin type I domain.
 CC :- SIMILARITY: Contains 2 kringle domains.

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DR EMBL; M23697; AAA41812.1; - .
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 DR EMBL; M31568; AAA42261

21-JUL-1986 (Rel. 01, Last sequence update)
15-NOV-2004 (Rel. 43, Last annotation update)
DT Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
DB (t-PA) (t-plasminogen activator) (Alteplase).
DE PLAT
RA Homo sapiens (Human), Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RA NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
TISSUE=Melanoma;
MEDLINE=83115242; PubMed=6337343;
RA Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A., Ward C.A., Bennett W.F., Goedel D.V., Collen D.,
RT "Cloning and expression of human tissue-type plasminogen activator cDNA in E. coli";
RN Nature 301:214-221 (1983).
[2] RN
SEQUENCE FROM N.A.
Tissue=Fetal lung;
MEDLINE=88262579; PubMed=31133640;
RA Sasai Y., Saito Y., Hayashi M., Otsuka K., Niwa M.;
RT "Nucleotide sequence of the tissue-type plasminogen activator from human fetal lung cells";
RN Nucleic Acids Res. 16:5655-5659 (1988).
[3] RN
SEQUENCE FROM N.A.
MEDLINE=88054470; PubMed=2824147;
RA Reddy V.B., Garramone A.J., Sasaki H., Wei C.-M., Watkins P., Galli J.,
RA Hsiung N.;
RT "Expression of human uterine tissue-type plasminogen activator in mouse cells using BPV vectors";
DNA 6:461-472 (1987).
[4] RN
SEQUENCE FROM N.A.
MEDLINE=86196143; PubMed=3009482;
RA Friezner Degen S.J., Rajput B., Reich B.;
RT "The human tissue plasminogen activator gene";
J. Biol. Chem. 261:6972-6985 (1986).
[5] RN
SEQUENCE FROM N.A.
MEDLINE=94298137; PubMed=6089198;
NY T., Eligh P., Lund B.;
RT "The structure of the human tissue-type plasminogen activator gene: correlation of intron and exon structures to functional and structural domains";
Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359 (1984).
[6] RN
SEQUENCE FROM N.A.
MEDLINE=16284200; PubMed=3090401;
RA Harris T.J., Patel T., Marston P.A., Little S., Emtage J.S.,
RA Opdenakker G., Volckaert G., Rombaerts W., Billiau A., Somer P.;
RT "Cloning of cDNA coding for human tissue-type plasminogen activator and its expression in *Escherichia coli*";
Mol. Biol. Med. 3:279-292 (1986).
[7] RN
SEQUENCE FROM N.A. (ISOFORM SHORT).
Tissue=Umbilical vein;
MEDLINE=201922129; PubMed=2107528;
RA Siebert P.D., Fong K.;
RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from human endothelial cells";
Nucleic Acids Res. 18:1086-1086 (1990).
[8] RN
SEQUENCE FROM N.A.
Tissue=brain;
MEDLINE=22188257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schaefer C.P., Duschner N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA RT Biochemistry 30:2311-2314 (1991).
RN DISULFIDE BONDS IN KRINGLE 2;
RP MEDLINE=91444765; PubMed=1645316;
RA RT Biochemistry 30:2311-2314 (1991).
RN DISULFIDE BONDS IN KRINGLE 2;
RP MEDLINE=9159408; PubMed=190441;
RA RT Biochemistry 30:2311-2314 (1991).
RN DISULFIDE BONDS IN KRINGLE 2;
RP MEDLINE=90992112; PubMed=2131016;
RC TISSUE=Melanoma;
RA MEDLINE=83109620; PubMed=6682760;
RA Pohl G., Keijlsvoet M., Bergsorf N., Wallen P., Joernvall H.;
RT "Tissue plasminogen activator: Peptide analyses confirm an indirectly derived amino acid sequence, identify the active site serine residue, establish glycosylation sites, and localize variant differences";
RT "Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells";
J. Biol. Chem. 260:11223-11230 (1985).
[11] RN
SEQUENCE OF 31-562 FROM N.A.
RX MEDLINE=91291340; PubMed=1168681;
RA Itagaki Y., Yasuda S., Morinaga T., Mitsuda S., Higashio K.;
RT "Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells";
Agric. Biol. Chem. 55:1225-1232 (1991).
[12] RN
SEQUENCE OF 31-562 FROM N.A.
RX MEDLINE=91291340; PubMed=1168681;
RA Itagaki Y., Yasuda S., Morinaga T., Mitsuda S., Higashio K.;
RT "Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells";
Agric. Biol. Chem. 55:1225-1232 (1991).
[13] RN
SEQUENCE OF 36-562.
RX TISSUE=Melanoma;
RA MEDLINE=85000468; PubMed=6433976;
RA Pohl G., Keijlsvoet M., Bergsorf N., Wallen P., Joernvall H.;
RT "Tissue plasminogen activator: Peptide analyses confirm an indirectly derived amino acid sequence, identify the active site serine residue, establish glycosylation sites, and localize variant differences";
RT "Purification and characterization of a melanoma cell plasminogen activator";
RL Eur. J. Biochem. 132:681-686 (1983).
[14] RN
STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=90992112; PubMed=2131016;
RC TISSUE=Melanoma;
RA MEDLINE=83109620; PubMed=6682760;
RA Wallen P., Pohl G., Bergsorf N., Raanby M., Ny T., Joernvall H.;
RT "Carbohydrate structure of recombinant human uterine tissue plasminogen activator expressed in mouse epithelial cells";
RT "Plasminogen activator expressed in mouse epithelial cells";
RL Eur. J. Biochem. 186:273-286 (1989).
[15] RN
CARBOHYDRATE-LINKAGE SITE THR-396.
RX MEDLINE=9159408; PubMed=190441;
RA Harris R.J., Leonard C.K., Guzetta A.W., Spellman M.W.;
RA RT "Tissue plasminogen activator has an O-linked fucose attached to Threonine-61 in the epidermal growth factor domain";
RT Biochemistry 30:2311-2314 (1991).
RN DISULFIDE BONDS IN KRINGLE 2;
RP MEDLINE=91444765; PubMed=1645316;

RA	Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.; "Disulfide pairing of the recombinant kringle-2 domain of tissue plasminogen activator produced in Escherichia coli.";
RT	
RL	J. Biol. Chem. 266:10070-10072(1991).
RN	[17]
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
RX	MEDLINE=90200985; PubMed=8613982;
RA	Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U., Bode W.;
RA	"The 2.3 Å crystal structure of the catalytic domain of recombinant RT two-chain human tissue-type plasminogen activator.";
RL	J. Mol. Biol. 258:1117-1135(1996).
RN	[18]
RP	X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
RX	MEDLINE=97449126; PubMed=9305622;
RA	Renatus M., Engl R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U., Bode W.;
RA	"Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray crystal structure of single-chain human tPA.";
RL	EMBO J. 16:4797-4805(1997).
RN	[19]
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
RX	MEDLINE=92118803; PubMed=1310033;
RA	de Vos A., Ultach M.H., Kelley R.F., Padmanabhan K., Tulinsky A., Westbrook M.L., Kossiakoff A.A.;
RA	"Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4-Å resolution.";
RT	Biochemistry 31:270-279(1992).
RN	[20]
RP	STRUCTURE BY NMR OF KRINGLE 2.
RX	MEDLINE=90122799; PubMed=2558718;
RA	Byeon I.-J.L., Kelley R.F., Linas M.; "1H NMR structural characterization of a recombinant kringle 2 domain from human tissue-type plasminogen activator.";
RT	Biochemistry 28:9356-9360(1989).
RN	[21]
RP	STRUCTURE BY NMR OF KRINGLE 2.
RX	MEDLINE=91200042; PubMed=1901289;
RA	Byeon I.-J.L., Kelley R.F., Linas M.;
RT	"Kringle-2 domain of the tissue-type plasminogen activator. 1H-NMR assignments and secondary structure.";
RL	Eur. J. Biochem. 197:155-165(1991).
RN	[22]
RP	STRUCTURE BY NMR OF KRINGLE 2.
RX	MEDLINE=9216329; PubMed=1762144;
RA	Byeon I.-J.L., Linas M.;
RT	"Solution structure of the tissue-type plasminogen activator kringle 2 domain complexed to 6-aminohexanoic acid an antifibrinolytic drug.";
RT	J. Mol. Biol. 222:1035-1051(1991).
RN	[23]
Query Match	5.2%; Score 13; DB 1; Length 562;
Best Local Similarity	100.0%; Pred. No. 1.4e-05;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	507 DACQDSSGGPLVC 519
RESULT 12	
TPA_BOVIN	STANDARD; PRT; 566 AA.
AC	Q28198;
DT	01-NOV-1997 (Rel. 35, Created)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DB	Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA) (t-PA) (t-plasminogen activator).
DB	PLAT.
GN	Bos caurus (Bovine).
OS	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota;

OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovine; Bos. NCBTaxID=9913;
OC	SEQUENCE FROM N.A.
OX	[1]
RN	RP
RC	TISSUE=Kidney;
RA	Ravn P., Berglund L., Petersen T.B.;
RA	"Cloning and characterization of the bovine plasminogen activators uPA and tPA.";
RT	Int. Dairy J. 5:605-617(1995).
RT	"The abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling Plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events.
CC	-1- CATALYTIC ACTIVITY: Specific cleavage of Arg- -Val bond in plasminogen to form plasmin.
CC	-1- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide bond.
CC	-1- SUBCELLULAR LOCATION: Secreted; extracellular.
CC	-1- PIM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZMB, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
CC	-1- MISCELLANOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.
CC	-1- SIMILARITY: Belongs to peptidase family SI.
CC	-1- SIMILARITY: Contains 1 EGF-like domain.
CC	-1- SIMILARITY: Contains 2 kringle domains.
CC	-1- SIMILARITY: Contains 2 kringle domains.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; X85800; CMA59795.1; -.
DR	HSSP; P00750; 1RTP.
DR	MEROPS; S01_232; -.
DR	InterPro; IPR009003; Cys_Ser_trypsin.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR000083; Fibronectin.
DR	InterPro; IPR006210; IEGF.
DR	InterPro; IPR001254; Kringle.
DR	InterPro; IPR001314; Peptidase_SI.
DR	Pfam; PF00008; BGP; 1.
DR	Pfam; PF00039; fnl; 1.
DR	Pfam; PF00051; kringle; 2.
DR	Pfam; PF00089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR0018; KRINGLE.
DR	ProDom; PD00035; Kringle; 2.
DR	SMART; SM00181; EGF; 1.
DR	SMART; SM0058; fnl; 1.
DR	SMART; SM00130; KR; 2.
DR	PROSITE; PS00020; TRYSP; SPC; 1.
DR	PROSITE; PS00022; EGF; 1; 1.
DR	PROSITE; PS01186; EGF_-2; 1.
DR	PROSITE; PS50026; EGF; 3; 1.
DR	PROSITE; PS01253; FIBROECTIN_1; 1.
DR	PROSITE; PS00021; KRINGLE_-1; 1.
DR	PROSITE; PS50070; KRINGLE_2; 2.
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; repeat; signal.
FT	SIGNAL; 1 21 BY SIMILARITY.
FT	PROPEP 22 33 BY SIMILARITY.
FT	CHAIN 34 566 TISSUE-TYPE PLASMINOGEN ACTIVATOR.

		TISSUE-TYPE PLASMINOGEN ACTIVATOR A			TISSUE-TYPE PLASMINOGEN ACTIVATOR B		
	CHAIN	34	314	566	82	121	209
PT	CHAIN	315	566				
PT	DOMAIN	40					
PT	DOMAIN	83					
PT	DOMAIN	128					
PT	DOMAIN	219					
PT	DOMAIN	315					
FT	ACT SITE	361					
FT	ACT SITE	361					
FT	ACT SITE	410					
FT	ACT SITE	517					
FT	DISULPID	42					
FT	DISULPID	70					
FT	DISULPID	87					
FT	DISULPID	92					
FT	DISULPID	111					
FT	DISULPID	128					
FT	DISULPID	149					
FT	DISULPID	180					
FT	DISULPID	219					
FT	DISULPID	240					
FT	DISULPID	271					
FT	DISULPID	303					
FT	DISULPID	346					
FT	DISULPID	354					
FT	DISULPID	448					
FT	DISULPID	480					
FT	DISULPID	513					
FT	CARBHYD	153					
FT	CARBHYD	487					
AA	SEQUENCE	566					
AA	SEQUENCE	63701					
MW;							
ISQ							

Qy 194 DACCGDSGGGLYC 206
DCCGDSGGGLYC 206
DCCGDSGGGLYC 206
DCCGDSGGGLYC 206

RESULT 1.3					
	FA1.2	BOVIN	STANDARD;	PRT;	593 AA.
ID	PA12	BOVIN			
AC	P98140;				
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	15-MAR-2004	(Rel. 43, Last annotation update)			
DE	Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)				

F12. *Bos taurus* (Bovine).
Eukaryota; *Metazoa*; *Chordata*; *Craniata*; *Vertebrata*; *Butelostomi*; *Mammalia*; *Bentharia*; *Cetartiodactyla*; *Ruminantia*; *Pecora*; *Bovidae*; *Bovinae*; *Bos*.
 NCBI_TaxID=9913;
 [1]
 SRQEN
 RPRP
 LOCOS
 TISSUE=Liver;
 PubMed=8186251;
 MBDLINE=94242782;
 Shibusawa Y., Saito U., Okabe H., Kambara T., Yamamoto T.; "Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human Hageman factor (blood coagulation factor XI)." Biochim Biophys Acta 1206:63-70(1994).

[2] RRP SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDLINE=77182112; PubMed=861210;
RX RA Pujikawa K., Walsh A.K., Davie W.B.;
RA "isolation and characterization of bovine factor XII (Hageman
factor)";
RT RT Biochem Biophys Res Commun 16:2270-2272(1977).
CCC |- FUNCTION: Factor XII is a serum glycoprotein that participat

Que B.G., Davie E.W.;	Characterization of a cDNA coding for human factor XII (Hageman factor);
RT	Biochemistry 25:1525-1528 (1986).
[6]	
RT	SEQUENCE OF 20-379; PubMed=388654;
RP	MBIDLINE=85182674; PubMed=388654;
RT	McMullen B.A., Fujikawa K.;
RT	"Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated Hageman factor).";
RT	J. Biol. Chem. 260:5328-5341(1985).
[7]	
RT	SEQUENCE OF 354-362 AND 373-315;
RP	MBIDLINE=85182674; PubMed=388654;
RT	Schloesser M., Hoffert S., Bartz U., Lamme B., Engel W.
RA	"The novel acceptor splice site mutation 11396(G->A) in the factor XII gene causes a truncated transcript in cross-reacting material negative patients.,"
RA	Hum. Mol. Genet. 4:1235-1237(1995).
[8]	
RT	CARBOHYDRATE-LINKAGE SITE THR-109.
RP	MBIDLINE=92184750; PubMed=1544894;
RC	Harris R.J., Ling V.T., Spellman M.W.;
TISSUE=Blood;	"O-linked fucose is present in the first epidermal growth factor domain of factor XII but not protein C.,"
RX	J. Biol. Chem. 267:5102-5107(1992).
[9]	
RT	VARIANT WASHINGTON D.C. SER-190.
RP	MBIDLINE=9046788; PubMed=2510163;
RX	Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
RA	Saito H.;
RA	"Coagulation factor XII (Hageman Factor) Washington D.C.: inactive factor XII results from Cys-571-->Ser substitution.,"
RT	Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
[10]	
RT	VARIANT LOCARNO PRO-372.
RP	MBIDLINE=94325559; PubMed=8049433;
RX	Kondo S., Tokunaga F., Kawano S., Koide T., Furukawa M., Hovinga J.K., Schaller J., Stricker H., Wuillemin W.A., Laemmle B.;
RA	"Coagulation factor XII Locarno: the functional defect is caused by the amino acid substitution Arg-353-->Pro leading to loss of a kallikrein cleavage site.,"
RT	Blood 84:1173-1181(1994).
[11]	
RT	VARIANT TENRI CYS-53.
RP	MBIDLINE=9290785; PubMed=10161128;
RX	Kondo S., Tokunaga F., Kawano S., Ono Y., Kumagai S., Koide T., Riedler M.J., Armel T.Z., Carrington D.P., Oruna M., Kuldaneck S. A., Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
[12]	
RT	SEQUENCE OF 4-615 FROM N.A.
RP	MBIDLINE=8603330; PubMed=38707053;
RX	Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D., Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A., Cortese R.;
RA	"cDNA sequence coding for human coagulation factor XII (Hageman).";
RT	Nucleic Acids Res. 14:3146-3146 (1986).
[4]	
RT	SEQUENCE OF 14-615 FROM N.A.
RP	MBIDLINE=86176794; PubMed=3754331;
RX	Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D., McGillicuddy R.T.A.;
RA	"Characterization of human blood coagulation factor XII cDNA. Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XII.,"
RT	J. Biol. Chem. 260:13666-13676 (1985).
[5]	
RT	SIMILARITY: Belongs to peptidase family S1.
CC	- - CATALYTIC ACTIVITY: Cleaves selectively Arg-[Ile bonds in factor XII to form factor VIIa and factor XI to form factor XIIa.
CC	- - PTM: O- AND N-GLYCOSYLATION.
CC	- - DISEASE: Defects in FI1 do not cause any clinical symptoms. The sole effect is that whole-blood clotting time is prolonged.
CC	- - MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor XIIa activates factor XI to factor XIIa.
CC	- - SIMILARITY: Contains 1 fibronectin type I domain.
CC	- - SIMILARITY: Contains 1 fibronectin type I domain.

-1- SIMILARITY: Contains 1 fibronectin type II domain.
 CC -1- SIMILARITY: Contains 1 kringle domain.

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CC EMBL; M31315; AA70225; 1; -. DR MIM; 224000; DR Genew; HGNC; 3530; F12. DR GO; GO:0003805; F:Blood coagulation factor XI activity; TAS. DR GO; GO:0003806; F:Blood coagulation factor XII activity; TAS. DR GO; GO:0008236; F:serine-type Peptidase activity; TAS. DR InterPro; IPR009003; Cys_Ser_trypsin. DR InterPro; IPR006209; EGF_1-like. DR InterPro; IPR000083; Fibronectin. DR InterPro; IPR000562; FN_Type_II. DR InterPro; IPR006210; IEGP. DR InterPro; IPR000001; Kringle. DR InterPro; IPR001254; Peptidase_S1. DR InterPro; IPR001314; Peptidase_SIA. PRam; PR000039; fn1; 1. PRam; PR000040; fn2; 1. DR PRam; PR000051; Kringle; 1. DR PRam; PR000089; trypsin; 1. DR PRINTS; PR000722; CHYMOTRYPSIN. DR PRINTS; PR000113; FNTYBLLI. DR PRINTS; PR000118; KRINGLB. DR ProdDom; PD000995; FN_Type_II; 1. DR SMART; SM000395; Kringle; 1. DR SMART; SM00181; EGF; 2. DR SMART; SM00058; FN1; 1. DR SMART; SM00059; FN2; 1. DR SMART; SM00130; FR; 1. DR SMART; SM00020; TRYD_SPC; 1. DR PROSITE; PS0002; KRINGLE_1; 2. DR PROSITE; PS01186; EGF_1; 1. DR PROSITE; PS50026; EGF_3; 2. DR PROSITE; PS00053; FIBRONECTIN_1; 1. DR PROSITE; PS00023; FIBRONECTIN_2; 1. DR PROSITE; PS5007; KRINGLE_2; 1. DR PROSITE; PS50240; TRYPSIN_DOM; 1. DR PROSITE; PS00134; TRYPSIN_HIS; 1. DR PROSITE; PS00135; TRYPSIN_SER; 1. KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine_protease; KW Hydrolase; Fibrinolysis; Signal; EGP-like domain; Repeat; Zymogen; KW Polymorphism; Disease mutation.

SIGNAL 1 19 FT CHAIN 20 372 ALPHA-FACTOR_XIIA_HEAVY_CHAIN. FT CHAIN 373 615 ALPHA-FACTOR_XIIA_LIGHT_CHAIN. FT CHAIN 354 362 BETA-FACTOR_XIIA_PART_1. FT CHAIN 373 615 BETA-FACTOR_XIIA_PART_2. FT DOMAIN 47 88 FIBRONECTIN_TYPB-II. FT DOMAIN 94 131 EGF-LIKE_1. FT DOMAIN 133 173 FIBRONECTIN_TYPB-II. FT DOMAIN 210 210 EGF-LIKE_2.

Qy	1 MGLSIPILLCVGLSQAAATPKIENGTECGRNSQPWQVLFPGTSLRCGGVLIDHRWLVTA 60	194 DACQDGSGGPLVCGVTLQGLVSGSYGPGCQ 224
Db	1 MGLSIPILLCVGLSQAAATPKIENGTECGRNSQPWQVLFPGTSLRCGGVLIDHRWLVTA 60	180 DACQDGSGGPLVCGVTLQGLVSGSYGPGCQ 210
Qy	61 AHCSG 65	
Db	61 AHCSG 65	
RESULT 2		
Q9CV76	PRELIMINARY;	PRT; 234 AA.
ID	Q9CV76; 01-JUN-2001 (T-EMBLrel. 17, Created)	
AC	DT 01-OCT-2003 (T-EMBLrel. 17, Last sequence update)	
AC	DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)	
AC	DB 2310008B01RIK protein (Fragment).	
OS	Mus musculus (Mouse)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
STRAIN=C57BL/6J; TISSUE=Tongue; MEDLINE=21:085680; PubMed=11218851;	SEQUENCE FROM N.A.	
RA	Kawai J., Shingawa K., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki T., Boni H., Kabusawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pebble G., Quackenbush J., Schriml L.M., Staubli R., Suzuki R., Tonita M., Wagner L., Washio T., Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Ballez J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hueme D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mazzarelli J., Sakamoto N., Nordone P., Ring B., Rodriguez I., Storch K.-F., Sasak H., Sato K., Schoenbach C., Seiya T., Shibata Y., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittraker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Hayashizaki Y.	
RT	"Functional annotation of a full-length mouse cDNA collection." Nature 409:685-690(2001).	
RL	CC :- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.	
DR	EMBL; AK00917; BAB26143.1; -.	
DR	HSSP; P00763; LP0.	
DR	MEROPS; S01_020; -.	
DR	MGD; MG:191676; 2310008B01RIK.	
DR	GO: GO:0004263; F:chymotrypsin activity; IEA.	
DR	GO: GO:0008233; F:peptidase activity; IEA.	
DR	GO: GO:000495; F:trypsin activity; IEA.	
DR	GO: GO:006508; F:proteolysis and peptidolysis; IEA.	
DR	InterPro: IPR009090; Cys_Ser_trypsin.	
DR	SMART: SM00020; Cys_Ser_trypsin.	
DR	PROSITE: PS00179; BGP_C4.	
DR	PROSITE: PS00020; TRYSPIN_SPC.	
DR	PROSITE: PS00070; ALDEHYDDB_DEHYDR_CYS; 1.	
DR	PROSITE: PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE: PS01180; CUB; 2.	
DR	PROSITE: PS01187; EGFB_C4.	
DR	PROSITE: PS50240; TRYPSIN_DOM; 1.	
DR	PROSITE: PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE: PS00135; TRYPSIN_SER; 1.	
KW	Lectin; Protease.	
SQ	SEQUENCE 681 AA; 75277 MW; 27386PA117CD437 CRC64;	
Qy	Query Match 5.6%; Score 14; DB 13; Length 681; Best Local Similarity 10.0%; Pred. No. 1.5e-05; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	192 QGDACGCGGSPFLV 205	
Qy	Best Local Similarity 100.0%; Pred. No. 1.1e-23; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	622 QGDACGCGGSPFLV 635	

RESULT 4				
Q92416	ID Q92416 PRELIMINARY; PRT; 200 AA.			
AC	Q92416; PROTEIN; CHYMOTRYPSIN.			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DB	Serine protease-like 1.			
GN	170036D21RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RL	"Mus" muscular mRNA for serine protease-like gene spliced variant-1.			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.				
DR	EMBL: AB047758; BAB63919.1; -.			
DR	HSSP: P00761; LAN1.			
DR	MEROPS; SOL106; -.			
DR	MGD; MGI:1920586; 1700036D21RIK.			
DR	GO:0004263; P:chymotrypsin activity; IEA.			
DR	GO:0008233; P:peptidase activity; IEA.			
DR	GO:0004295; P:trypsin activity; IEA.			
DR	GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR00903; Cys Ser_trypsin.			
DR	InterPro; IPR001254; Peptidase_S1.			
DR	InterPro; IPR001314; Peptidase_S1A.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SM00020; TRYPSIN_SPC; 1.			
DR	PROSITE; PS00135; TRYPSIN_DOM; 1.			
KW	Hydrolase; Protease; Serine protease.			
SEQUENCE 200 AA;	972959B468BF603 CRC64;			
Query Match	5.2%; Score 13; DB 11; Length 200;			
Best Local Similarity	100.0%; Pred. No. 5.8e-05;			
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	194 DACQDGSGPLVC 206			
Db	128 DACQDGSGPLVC 140			
RESULT 5				
Q8N4E0	ID Q8N4E0 PRELIMINARY; PRT; 235 AA.			
AC	Q8N4E0; PROTEIN; CHYMOTRYPSIN.			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DB	Hypothetical protein (Fragment).			
OS	Hom sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=skin;			
RC	Strausberg R.;			
RC	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
DR	EMBL: BC034529; AA134529.1; -.			
DR	GO:0004263; P:chymotrypsin activity; IEA.			
DR	GO:0008233; P:peptidase activity; IEA.			
DR	GO:0004295; P:trypsin activity; IEA.			
DR	GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR00903; Cys Ser_trypsin.			
DR	InterPro; IPR001254; Peptidase_S1.			
DR	InterPro; IPR001314; Peptidase_S1A.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SM00020; TRYPSIN_SPC; 1.			
DR	PROSITE; PS50040; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	PROSTTB; PS00135; TRYPSIN_SER; 1.			
FT	NON TER 1			
SQ	SEQUENCE 242 AA;	26059 MW;	A3P8A624DE481D36 CRC64;	
Query Match	5.2%; Score 13; DB 11; Length 242;			
Best Local Similarity	100.0%; Pred. No. 6.9e-05;			
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Db	196 CGQDGSGPLVCGG 208			
Db	191 CGQDGSGPLVCGG 203			
RESULT 7				
Q867V5	ID Q867V5 PRELIMINARY; PRT; 243 AA.			
AC	Q867V5; PROTEIN; CHYMOTRYPSIN.			
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DB	Similar to D component of complement (Adipsin) (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OC	NCBI_TaxID:9606;			

RESULT 8
 Q8B301 ID PRELIMINARY; PRT; 246 AA.
 AC 08B301 PRELIMINARY; PRT; 246 AA.
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Serine protease (BSP).
 GN PRSS18 OR MBSP.
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1] RN SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RC STRAIN=BALB/C; TISSUE=Skin;
 RN Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RESULT 9
 Q9W7Q5 ID PRELIMINARY; PRT; 247 AA.
 AC 09W7Q5 PRELIMINARY; PRT; 247 AA.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Trypsinogen 3.
 OS Paralichthys olivaceus (Plounder).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
 OC Pleuronectoidei; Paralichthyidae; Paralichthys.
 OC NCBI_TaxID=8255;
 RN [1] RN SEQUENCE FROM N.A.
 RP TISSUE=Pancreas;
 RC Suzuki T., Srivastava A.S., Kurokawa T.;
 RT "Japanese flounder mRNA for trypsinogen 3."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RESULT 10
 QY 198 GDSGGPLVCGGVL 210
 DB 196 GDSGGPLVCGGVL 208

Query Match 5.2%; Score 13; DB 4; Length 243;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Oligos 0; Gaps 0;

Query Match 5.2%; Score 13; DB 11; Length 246;
 Best Local Similarity 100.0%; Pred. No. 7e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Oligos 0; Gaps 0;

Qy 196 CGDGGPLVCG 208
 Db 193 CGDGGSPLVCG 205

RESULT 11
 Q9W7Q5 ID PRELIMINARY; PRT; 247 AA.
 AC 09W7Q5 PRELIMINARY; PRT; 247 AA.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Trypsinogen 3.
 OS Paralichthys olivaceus (Plounder).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
 OC Pleuronectoidei; Paralichthyidae; Paralichthys.
 OC NCBI_TaxID=8255;

RESULT 12
 Q9W7Q5 ID PRELIMINARY; PRT; 247 AA.
 AC 09W7Q5 PRELIMINARY; PRT; 247 AA.
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Serine protease (BSP).
 GN PRSS18 OR MBSP.
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1] RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Matsui H., Takahashi T.;
 RT "Mouse serine protease preferentially expressed in brain."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

InterPro; IPR001314; Peptidase_SIA.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; TRYSPIN_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SRR; 1.
KW Hydrolase; Protease; Serine protease.
SEQUENCE 247 AA; 26348 MW; DC4B64179DD972 CRC64;
SQ STRAIN=N.A.; STRAIN=Sprague-Dawley;
MEDLINE=7477435; PubMed=9314391;
Best Local Similarity 100.0%; Pred. No. 7e-05; Length 247;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 194 DACKDGGCPLVC 206
Db 194 DACKDGGCPLVC 206
RESULT 10
Q8CCR5 PRELIMINARY; PRT; 250 AA.
ID Q8CCR5; GO:0004255; F:peptidase activity; IEA.
AC Q8CCR5; GO:0006508; P:proteolysis and peptidolysis; IEA.
DT 01-MAR-2003 (TREMBrel; 23; Created)
DT 01-MAR-2003 (TREMBrel; 23; Last sequence update)
DT 01-OCT-2003 (TREMBrel; 25; Last annotation update)
DE Glanular kallikrein KLK14.
GN OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] KLU14.
RN SEQUENCE FROM N.A.
MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y.; Lundahl A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
musculus."
RL Biochem Biophys Res Commun. 299:305-311(2002).
RP [2]
SEQUENCE FROM N.A.
RA Adams M.; Mural R.;
RL Submitted (SSP-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY152433; AN78421.1; -.
DR MGD; MGJ1:2447564; KLK14.
GO; GO:0004253; F:chymotrypsin activity; IEA.
DR GO; GO:0004255; F:trypsin activity; IEA.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; TRYSPIN_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SRR; 1.
SEQUENCE 250 AA; 27016 MW; F62RBB2290FEBB8 CRC64;
SQ STRAIN=N.A.; STRAIN=Sprague-Dawley;
MEDLINE=7477435; PubMed=9314391;
Best Local Similarity 100.0%; Pred. No. 7.1e-05; Length 250;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 196 CQGDSGGPLVCGG 208
Db 199 CQGDSGGPLVCGG 211
RESULT 12
Q8W2B4 PRELIMINARY; PPT; 253 AA.
ID Q8W2B4; GO:0004253; F:chymotrypsin activity; IEA.
AC Q8W2B4; GO:0006508; P:proteolysis and peptidolysis; IEA.
DT 01-MAR-2002 (TREMBrel; 20; Created)
DT 01-MAR-2002 (TREMBrel; 20; Last sequence update)
DT 01-OCT-2003 (TREMBrel; 25; Last annotation update)
DE Aliparin/Complement factor D precursor (EC 3.4.21.46).
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Reille M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AJ313463; CAC48304.1; -.
DR GO; GO:0004253; F:chymotrypsin activity; IEA.
DR HSSP; P0761; IAN1.
DR InterPro; IPR00903; Cys_Ser_trypsin.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR01314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
Qy 196 CQGDSGGPLVCGG 208
Db 199 CQGDSGGPLVCGG 211
RESULT 11
Q54854 PRELIMINARY; PRT; 251 AA.
ID Q54854; GO:0004253; F:chymotrypsin activity; IEA.
AC Q54854; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00903; Cys_Ser_trypsin.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR01314; Peptidase_S1A.

PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN SPC; 1.
DR PROSITE; PS00134; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN HIS; 1.
DR PROSITE; PS00135; TRYPSIN SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
PT SIGNAL 1 8
PT CHAIN 9 253 ADIPSIN/COMPLEMENT FACTOR D PRECURSOR.
SQ SEQUENCE 253 AA; 27033 MW; 78B06C209DEEA362 CRC64;

Query Match Score 13; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 QDGGPLVCGVL 210
Db 206 QDGGPLVCGVL 218

RESULT 13
ID Q91Y62 PRELIMINARY; PRT; 253 AA.
AC Q91Y62; PRELIMINARY; PRT; 253 AA.
DT 01-DRC-2001 (TrEMBLrel. 19, Created)
DT 01-OCT-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB Neurosin (Protease, serine, 18).
GN PRSS18.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buteraria; Primates; Catarrhini; Cercopitheciidae;
NCBI_TaxID=10200;
RN [1]_SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
DR AB046655; BAB03565.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.299; -.
DR GO; GO:0004263; P:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006505; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRTRNTS; PR00732; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS50040; TRYPSIN_DOM; 1.
DR PROSITE; PS00035; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 267 AA; 29516 MW; 69ACD18A0137AFC7 CRC64;

Query Match Score 13; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQQDGGPLVC 206
Db 159 DACQQDGGPLVC 171

RESULT 15
ID Q96899 PRELIMINARY; PRT; 277 AA.
AC Q96899; PRELIMINARY; PRT; 277 AA.
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB Plaaminogen activator subspainipes.
OS Scolopendra subspinipes.
CC Lukayota; Metazoa; Arthropoda; Myriapoda; Chilopoda; Scolopendra.
DR Pleurostigmophora; Scolopendromorpha; Scolopendridae; Scolopendra.
NCBI_TaxID=55038;
RN SBQDNCEB FROM N.A.
RA Sohn Y.-D.; You W.K.; Kim K.Y.; Chung K.H.; Park D.-H.;
RT "Cloning of a cDNA for a novel plasminogen activator from a Korean
RT centipede Scolopendra."
RL Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.
CC -I SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR U79521; AAD00320.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.122; -.
DR GO; GO:0004263; P:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.

Query Match Score 13; DB 11; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CGQDGGPLVCG 208
Db 200 CGQDGGPLVCG 212

DR GO: GO:0004295; F: trypsin activity; IEA.
DR GO; GO:0005508; P: proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; PepFidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR PFam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPTSPC; 1.
DR PROSITE; PS00020; TRIPSIN_DOM; 1.
DR PROSITE; PS00134; TRIPSIN_HIS; 1.
DR PROSITE; PS00135; TRXPNSN_SER; 1.
KW Hydrolase; Protease; Serine_protease.
SEQUENCE 277 AA; 30172 MW; EC62P80CBB246C CRC64;
SQ

Query Match 5.2%; Score 13; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQGDSGGPLVYC 206
||| ||| ||| ||| |||
Db 212 DACQGDSGGPLVYC 224

Search completed: June 16, 2004, 15:15:00
Job time : 48 secs